

## SEQUENCE LISTING

<110> Moyer, Richard W.

Li, Yi

<120> Materials and Methods for Delivery and Expression of Heterologous DNA in Vertebrate Cells

<130> UF-221C1XCZ1

<150> 09/086,651

<151> 1998-05-29

<150> 09/662,254

<151> 2000-09-14

<150> 60/224,479

<151> 2000-08-10

<160> 80

<170> PatentIn version 3.1

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&lt;400&gt; 2

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<213> Amsacta moorei entomopoxvirus

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<213> Amsacta moorei entomopoxvirus

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aataaaaca aatatactga ctataattca tcattaatta tgtcaaatgt ttataaaata	3240
tataataata aattggcatt aaataatata aattttaaaa tatcagaagg aaaatgtttt	3300
ggaattattg gtggtaacgg atgtggaaaa agtactattt ttaaaatatt atctggcgaa	3360
gaatgtgtta caaaaggaaa tatttatata ggatgttcta acagatcatg gatattaaaa	3420
tcaaattatt ttaaaaaaat atcttattgt tctcaatttt ttggcataga tacattttta	3480
acaggaagac aaaattttaa attaattatg atattaaatg gttttagtga taaacatata	3540
caatattata ttaatttttg gttaaaatta ttaaataatag aaaaatatgc agataaagca	3600

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gtttatacat acagtactgg tattataaaa cgtttaaaaa tagcaatgtc attagcacct 3660
agatcaatth taactttaat ggatgaacca acgtcaggaa tagatattgt atccaaacaa 3720
attatatgga aaactataaa atatattatt aattataatt attataatta ttacaaacat 3780
tccattttta tttcatcaaa taatatagaa gaaatagaat atttgtgctc taatgtgatt 3840
atcctagatt ctggaaatat aatgtataac gatactttgg aaaatattaa aaatatacat 3900
agtactaaaa taattaatat taaattatta cattatgata ataacaaaat ttgtaaaata 3960
aaaaataaat taaaaaataa aggtttttatg ttaaaatcag ataataaatt taaattaaca 4020
ttttgtgtat ctaaaaatat taatttgaaa tatagtgaat tatttaaaat attatatata 4080
ttaaagaata attattcaga tataattgat caatatgata taagtgatac aaatatagaa 4140
caattattht ca 4152

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<210> 10

<211> 236

<212> DNA

<213> Amsacta moorei entomopoxvirus

<400> 10

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atgaattatt acattttatt atgtctatth atgttattht catctagtta taatttttaa 60
ttaataaata ataatatthg taatgaagat tatgatcctg gaatatgtag aataggaata 120
ttagatggta ttataattat aatattaaag attgtaaaat atttattht ggtggatgtg 180
gtggtaacat gaataattht aataattatg aagattgtat taataaatgt ttaatt 236

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<210> 11

<211> 1719

<212> DNA

<213> Amsacta moorei entomopoxvirus

<400> 11

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atgaatatat atttaaaaaa tgcattcaat gatacaatat cgcattctgtc aaaatttaca 60
aatcaaataa atgatattat atcatthgat attaataatt ttactaaaaa tgthtttgatt 120

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atgcgtaata atattaataa tattagaact aattttgaaa atgtgtctga tgataatagt 180
ataaaaagaa gaataacaga attttttgat aaacaaaata cgccaaattt aaaattagga 240
agtataatat caattattaa atttcaacat ttaactgtaa catatgttaa taaaataata 300
aaagaaattg taacatataa atgtaatact agagaaataa atatagtaaa tttttcatct 360
gtcacatctc aaatttcaaa ctacgataat cctatattaa atgaaatatt aaaacaatat 420
gtatataaac aaaaattaaa aaatgttact gttaataatg ataaaaagaa aataattgat 480
cctgatgatg agaaattagc tgaatctatt aaaaaaatat tagaagaaat attaaaaata 540
ttattaatta taaaaaacia tgattgtgtt gcttatgggt catttacttg ttataatata 600
aatagaagta taaaatataa tgatatagat ttatatagta ctgatgcata tagaatttta 660
atatttttta tgatatatat acattttaact attggacatg acacttgttt atttagtata 720
ccttttataa ctgggcacat atcgttaaaa tataaaaaata tattttataat agattgtata 780
tttttagata attctattat aaatgttatt aataaatctt taattaataa tatatatattt 840
atagatcccg gtttaciaat gttaaataat tttagaatgt tatcagaaaa ttttagatct 900
tataaaatat atgaaaaaat ggaagaatct ttaaataaat ataaaacatt attaaattat 960
tttgtaata ataataataa atttaataaa caaagattaa attattgggt aaaatcagat 1020
gttgtagaa ataattttcc atatactata gtcgacaata caatattaat atcaataaaa 1080
gaattgatag atataagtcc atatgattat ataatgattg tattagattc gccgtcagac 1140
ataatggaaa aattatctaa tattagtggg ctatttagta gaaaatatgg tgctttttta 1200
aatgaaatat tttttgaaac aaaaaaaaata aaaaataaaa taaatacata tgctggaaac 1260
acaaataaca taacacaatt aattgatgaa aataaattaa taaaattaaa tagaagtgat 1320
ataaatatgc catataatat taatcccaat aagaaatatt taattttcag taatttaaca 1380
acatctacgt atgtttactt tgagaatgat aaaatgactg atatatcagt aaaaaatcta 1440
atatcattta tatcaacagc ttgtttatat aatttgttac acaaaaaaga tgattttgggt 1500
atggaattat attatttaac attacactgt cttacattta ccgaaactag aaaattaaat 1560
gaatataaag taatagatag atataaaaata aaaggcgaac ataaagaaat atcattgtgt 1620
aaaaatttat ttaattcaat atataaaaat aaaagtatgg aggacgaata tatggattat 1680
aatacattta tagatttaac taatataaat ggaggatat 1719

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<210> 12

&lt;211&gt; 286

&lt;212&gt; PRT

&lt;213&gt; Amsacta moorei entomopoxvirus

&lt;400&gt; 12

Met Thr Ile Phe Glu Ile Leu Ile Trp Ile Ile Val Leu Leu Ala Phe  
 1 5 10 15

Met Phe Ile Ile Phe Leu Tyr Val Val Leu Tyr Ile Lys Arg Arg Ile  
 20 25 30

Tyr Glu Ile Leu Asn Glu Asn Ile Pro Ile Glu Ile Asn Ile Asp Asn  
 35 40 45

Val Asn Tyr Pro Ser Glu Leu Tyr Thr Asp Lys Phe Asn Pro Asn Val  
 50 55 60

Leu Lys Tyr Leu Ile Lys Ile Leu Leu Asp Phe Asn Thr Glu Ile Thr  
 65 70 75 80

Asn Asn Ile Ile Ile His Ser Ile Asp Tyr Met Lys Ile Tyr Tyr Ile  
 85 90 95

Ser Tyr Asn Lys Lys Lys Ile Ile Lys Leu Ile Leu Asp Arg Tyr Asn  
 100 105 110

Asn Leu Trp Ile Val Ile Arg Gly Thr Leu Thr Tyr Asn Glu Phe Glu  
 115 120 125

His Asp Leu Arg Ile Ser Gln Val Lys Ile Asp Asn Cys Asp Met Lys  
 130 135 140

Cys His Lys Gly Phe Cys Glu Ile Tyr Ser Lys Ile Gln Lys Pro Leu  
 145 150 155 160

Leu Asn Leu Leu Met Thr Leu Ser Pro Asn Lys Ile Phe Ala Leu Gly  
 165 170 175

His Ser Leu Gly Gly Gly Ile Leu Ser Ile Ala Ala Tyr Asp Ile Phe  
 180 185 190

Asn Ile Leu Asn Lys Lys Glu Ile Ile Leu Tyr Thr Thr Gly Thr Pro  
 195 200 205

Arg Val Cys Asn Lys Asp Phe Tyr Asn Asn Cys Asn Lys Tyr Asn Ile  
 210 215 220

His Lys Val Glu Asn Leu Ser Asp Val Tyr Ile Asn Ala Ile Pro Ser  
 225 230 235 240

Val Leu Pro Phe Tyr Asp Asn Thr Val Tyr Tyr Lys Ile Gly Lys Ile  
 245 250 255

Trp Tyr Phe Asp Val Asn Tyr Gly Asn Ile Ile Leu His Lys Leu Glu  
 260 265 270

Ile Tyr Phe Asn Asn Ile Asp Asn Leu Lys Tyr Leu Glu Ile  
 275 280 285

<210> 13

<211> 151

<212> PRT

<213> Amsacta moorei entomopoxvirus

<400> 13

Met Lys Ala Ile Cys Val Met Thr Gly Lys Val Asn Gly Ile Ile Tyr  
 1 5 10 15

Phe Ile Gln Asn Ile Lys Gly Gly Ser Val His Val Lys Gly Lys Ile  
 20 25 30

Val Gly Leu Ser Lys Gly Leu His Gly Phe His Val His Glu Tyr Gly  
 35 40 45

Asp Val Ser Asn Gly Cys Thr Ser Ala Gly Glu His Phe Asn Pro Tyr  
 50 55 60

Asn Arg Gln His Gly Asp Ile Ser Asp Lys Ile His Arg His Val Gly  
 65 70 75 80

Asp Phe Gly Asn Val Tyr Ala Asp Glu Asn Gly Val Ala Asn Ile Asp  
85 90 95

Phe His Asp Asp Ile Ile Ser Leu Cys Gly Thr Asn Asn Ile Ile Gly  
100 105 110

Arg Thr Leu Val Val His Asp Ser Pro Asp Asp Leu Gly Lys Thr Asp  
115 120 125

Pro Leu Ser Lys Thr Ser Gly Asn Ser Gly Gly Arg Leu Gly Cys Gly  
130 135 140

Ile Ile Gly Ile Ala Lys Asp  
145 150

<210> 14

<211> 453

<212> PRT

<213> Amsacta moorei entomopoxvirus

<400> 14

Met Tyr Asn Asn Glu Tyr Phe Thr Asn Arg Val Lys Ile His Lys Lys  
1 5 10 15

Ile Asp Thr Ile Asn Lys Asn Val Leu Tyr Leu Ala Tyr Arg Asp Leu  
20 25 30

Arg Val Tyr Asp Asn Trp Ser Phe Leu Tyr Ser Gln Asn Ile Ala Tyr  
35 40 45

Leu Asn Asn Ser Ser Met Tyr Val Leu Tyr Leu Ile Asn Lys Asn Asn  
50 55 60

Asn Ile Asn Ile Arg Gln Tyr Lys Phe Leu Tyr Glu Gly Leu Pro Glu  
65 70 75 80

Phe Glu Ser Gln Cys Lys Lys Cys Asn Val Ser Phe His Leu Leu Ser  
85 90 95

Tyr Asn Asn Asn Ile Ile Ser Asn Phe Ile Asn Lys Tyr Lys Ile Gly

100					105					110					
His	Val	Ile	Ile	Glu	Gln	Met	Pro	Leu	Leu	Phe	His	Lys	Lys	Tyr	Tyr
		115					120					125			
Leu	Asp	Pro	Leu	Lys	Lys	Leu	Asn	Val	Asn	Val	Tyr	Ile	Val	Asp	Ser
	130					135					140				
His	Asn	Ile	Ile	Pro	Val	Trp	Val	Thr	Ser	Asp	Lys	Gln	Glu	Tyr	Asn
145					150					155					160
Ala	Arg	Thr	Ile	Arg	Ile	Lys	Ile	Asn	Lys	Leu	Lys	Asp	Gln	Tyr	Leu
				165					170					175	
Ile	Glu	Phe	Pro	Lys	Val	Lys	Ile	Ser	Asn	Ile	Gln	Pro	Ile	Phe	Val
			180					185					190		
Glu	Asn	Asn	Phe	Asp	Ile	Ile	Pro	Asn	Tyr	Asp	Lys	Lys	Leu	Ile	Asn
	195						200					205			
Ile	Tyr	Glu	Ile	Val	Gly	Gly	Tyr	Thr	Asn	Gly	Ile	Asn	Arg	Met	Asn
	210					215					220				
Asn	Phe	Phe	Lys	Asn	Lys	Ile	Asn	Thr	Tyr	Lys	Asp	Lys	Lys	Asn	Asn
225					230					235					240
Pro	Asn	Tyr	Glu	Asn	Thr	Ser	Ile	Leu	Ser	Pro	Trp	Leu	His	Cys	Gly
				245					250					255	
Met	Ile	Ser	Ala	Gln	Arg	Cys	Val	Leu	Glu	Ala	Asn	Lys	Leu	Lys	Lys
			260					265					270		
Ile	Lys	Asp	Tyr	Asn	Ile	Glu	Ser	Ile	Asp	Ser	Phe	Ile	Glu	Glu	Ile
		275					280					285			
Phe	Ile	Arg	Lys	Glu	Leu	Ser	Asp	Asn	Phe	Cys	Tyr	Tyr	Asn	Asn	Asn
	290					295					300				
Tyr	Lys	Ser	Phe	Ala	Ser	Cys	Pro	Asn	Trp	Ala	Ile	Leu	Thr	Leu	Glu
305					310					315					320
Ile	His	Lys	Thr	Asp	Lys	Arg	Asn	Lys	Ile	Phe	Ser	Leu	Arg	Glu	Leu
				325				330						335	

Glu Tyr Gly Lys Thr Asp Asn Lys Leu Trp Asn Tyr Cys Gln Tyr Tyr  
                   340                                  345                                  350

Leu Leu Lys Phe Gly Tyr Leu Asn Gly Tyr Met Arg Met Phe Trp Ala  
                   355                                  360                                  365

Lys Lys Leu Ile Glu Trp Thr Asn Ser Pro Gln Asp Ala Ile Asp Lys  
                   370                                  375                                  380

Thr Ile Tyr Leu Asn Asp Lys Tyr Phe Phe Asp Gly Tyr Asp Pro Met  
                   385                                  390                                  395                                  400

Gly Tyr Val Asn Ile Leu Trp Ser Ile Gly Gly Leu His Asp Arg Ala  
                                   405                                  410                                  415

Phe Lys Glu Arg Glu Met Tyr Gly Lys Ile Arg Phe Met Ser Gln Pro  
                                   420                                  425                                  430

Leu Met Tyr Lys Lys Leu Asn Val Asn Asp Phe Tyr Asn Asn Phe Asp  
                   435                                  440                                  445

Asn Val Ile Lys Ser  
                   450

<210> 15

<211> 263

<212> PRT

<213> Amsacta moorei entomopoxvirus

<400> 15

Met Met Asp Asp Ile Asn Leu Tyr Asn Glu Ser Glu Arg Leu Gln Thr  
   1                  5                                  10                                  15

Phe Glu Asn Trp Pro Ile Asn Phe Ile Thr Pro Glu Ser Phe Ala Ser  
                   20                                  25                                  30

Asn Gly Phe Tyr Tyr Ile Gly Glu Asn Asp Thr Val Lys Cys Val Tyr  
                   35                                  40                                  45

Cys Gly Val Gln Ile Asn Lys Trp Val Glu Gly Asp Lys Pro Glu Ile  
 50 55 60

Asp His Lys Lys Phe Ser Pro Asn Cys Ser Phe Leu Lys Ser Asn Asp  
 65 70 75 80

Gly Ile Asp Glu Cys Gly Asn Asn Lys Asn Ile Ser Asn Ile Thr Gln  
 85 90 95

Lys Gly Ala Val His Pro Asn Leu Ser Asn Ile Val Glu Arg Leu Lys  
 100 105 110

Thr Tyr Lys Glu Trp Pro Ile Ser Met Pro Ile Ser Thr Glu Lys Leu  
 115 120 125

Glu Ala Gly Phe Phe Tyr Thr Gly Lys Ser Asp Lys Val Lys Cys Phe  
 130 135 140

Tyr Cys Asp Gly Gly Leu Asn Lys Trp Glu Thr Asp Asp Asp Pro Trp  
 145 150 155 160

Ile Gln His Ala Arg Trp Phe Asp Lys Cys Asp Tyr Val Lys Leu Val  
 165 170 175

Lys Gly Lys Asp Phe Ile Gln Lys Val Met Thr Gln Ser Thr Phe Ile  
 180 185 190

Lys Ser Ser Lys Lys Glu Asn Ile Pro Glu Ile Asn Ile Ser Asn Asp  
 195 200 205

Glu Lys Asn Asp Ile Lys Leu Cys Lys Ile Cys Tyr Ile Glu Glu Arg  
 210 215 220

Val Ile Cys Phe Val Pro Cys Gly His Ile Phe Cys Cys Gly Lys Cys  
 225 230 235 240

Ala Ile Ser Met Asp Lys Cys Pro Val Cys Arg Asn Lys Ile Lys Asn  
 245 250 255

Leu Thr Arg Val Tyr Tyr Pro  
 260

&lt;210&gt; 16

&lt;211&gt; 295

&lt;212&gt; PRT

&lt;213&gt; Amsacta moorei entomopoxvirus

&lt;400&gt; 16

Met Asn Phe Met Pro Gln Tyr Tyr Tyr Ile Ser Asp Ile Asn Asn Glu  
 1 5 10 15

Ile Glu Tyr Asp Glu Asn Phe Asn Pro Gly Lys Lys Phe Asp Phe Lys  
 20 25 30

Arg Gln Gly Gln Ile Lys Leu Leu Met Asn Glu Ile Arg Phe Leu Thr  
 35 40 45

Glu Asp Val Glu Leu His Lys Asn Tyr Lys Asn Glu Asn Ile Asn Ile  
 50 55 60

Leu Tyr Ile Gly Ser Gly Lys Gly Tyr His Ile Pro Leu Leu Ile Asn  
 65 70 75 80

Met Tyr Ser Asp Tyr Lys Ile Gln Trp Asp Leu Tyr Asp Pro Cys Gly  
 85 90 95

His Cys Glu Lys Leu Tyr Asn Ile Gln Lys Asn Asn Asn Asn Ile Lys  
 100 105 110

Ile Tyr Asp Thr Tyr Phe Asn Lys Ser Asp Val Glu Lys Tyr Glu Asn  
 115 120 125

Ile Asp Asn Leu Leu Phe Ile Thr Asp Ile Arg Thr Val Asp Asn Pro  
 130 135 140

Asp Asp Glu Pro Asn Thr Lys Asn Leu Ile Asn Asp Tyr Glu Leu Gln  
 145 150 155 160

Asn Tyr Ile Leu Lys Glu Leu Lys Pro Ile Ser Leu Val Lys Gln Arg  
 165 170 175

Asp Pro Phe Pro Asn Asp Trp Asp Asp Ser Tyr Lys Leu Ser Ile Pro



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180              185              190
Asp Gly Lys Glu Tyr Ile Gln Cys Phe Gln Lys Tyr Asn Ser Ala Glu
    195              200              205

Tyr Arg Ile Phe Ile Ser Gly Ile Thr Thr Phe Val Asp Ile Asn Ser
    210              215              220

Val Ile Leu Asn Lys Arg Gly Ile Asp Arg Lys Leu Ala Trp Tyr Asn
    225              230              235              240

Met Lys Tyr Arg Phe Gln Asn Asp Asn Asp Tyr Lys Ile Ala Tyr Arg
    245              250              255

Ile Leu Asn Lys Tyr Ile Lys Ser Glu Asn Lys Pro Ile Leu Lys Lys
    260              265              270

Tyr Asn Asn Ile Asn Lys Asn Asn Ile Lys Asn Val Ile Arg Ser Leu
    275              280              285

Ser Lys Glu Met Gly Tyr Tyr
    290              295

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<210> 17

<211> 292

<212> PRT

<213> Amsacta moorei entomopoxvirus

<400> 17

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Met Asp Val Asn Lys Tyr Ile Tyr Glu Tyr Asn Lys Pro Leu Tyr Tyr
1              5              10              15

Thr Tyr Tyr Asp Leu Cys Arg Asn Met Asn Asp Val Ile Tyr Asp Tyr
    20              25              30

Asn Asn Asn Thr Ile Lys Lys Tyr Met Asp Ile Leu Leu Ser Gln Ile
    35              40              45

Gln Phe Leu Ser Asn Ile Asn Ile Lys Lys Ile Cys Asn Asn Thr Asn
    50              55              60

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Gly Ile Val Asn Ile Leu Tyr Ile Gly Ser Ser Lys Ala Tyr His Phe  
65 70 75 80

Asn Ile Leu Asn Glu Leu Tyr Lys Asn Leu Thr Asn Ile Gln Trp Tyr  
85 90 95

Phe Tyr Asp Ile Ile Asp Pro Cys Ile Ser Val Glu Arg Leu Ser Tyr  
100 105 110

Asn Ile Ile Phe Asn Arg Leu Phe Thr Glu Asp Asp Ile Ile Asp Phe  
115 120 125

Lys Asp Lys Tyr Pro Leu Ile Leu Ile Tyr Asp Tyr Asp Asp Lys Ser  
130 135 140

Asn Val Arg Asp Leu Leu Tyr His Tyr Asn Met Gln Asn Asn Ile Ile  
145 150 155 160

Ile Tyr Leu Asn Pro Thr Tyr Ser Leu Leu Lys Phe Lys Tyr Met Pro  
165 170 175

Ile Asn Lys Trp Asn Asn Ser Phe Asn Asp Tyr Glu Tyr Ile Ser Thr  
180 185 190

Gly Ile Lys Tyr Leu Pro Thr Ile Lys Ser Leu His Thr Arg Asn Ile  
195 200 205

Ile Asp Asn Lys Asn Ile Met Thr Leu Thr Phe Asp Glu Ile Glu Ser  
210 215 220

Glu Asn Tyr Tyr Glu Lys Met Asn Tyr Tyr Asn Asn Cys Ser Gly Tyr  
225 230 235 240

Asn Asp Ile Tyr Asn Asn Ile Ser Gly Tyr Ile Leu Asn Lys Ser Asn  
245 250 255

Leu Tyr Asp Asn Asn Asn Ser Ala Tyr Asn Ile Leu Lys Ile Tyr Glu  
260 265 270

Lys Asn Ile Ile Asn Thr Ile Asn Glu Asp Lys Ile Phe Arg Ser Lys  
275 280 285

Glu Lys Tyr Ile  
290

<210> 18

<211> 1089

<212> PRT

<213> Amsacta moorei entomopoxvirus

<400> 18

Met Pro Phe Leu Gly Thr Gly Ile Leu Lys Phe Asp Ile Thr Gln Leu  
1 5 10 15

Gln Asn Lys Glu Lys Gly Ser Asp Tyr Asn Ala Ile Arg Tyr Leu Lys  
20 25 30

Arg Ile Leu Asn Lys Pro Cys Asp Asn Asp Asp Ile Leu Ile Pro Tyr  
35 40 45

Asp Lys Leu Glu Ser Lys Glu Ile Asn Ile Ile Tyr Asn Trp Tyr Ile  
50 55 60

Ile Lys Pro Ser Ser Leu Glu Gln Phe Ile Val Cys Lys Cys Lys Asp  
65 70 75 80

Tyr Asp Thr Glu Glu Ile Ile Tyr Ile Leu Phe Asp Ile Tyr Glu Tyr  
85 90 95

Phe Leu Cys Asp Tyr Glu Leu Ser Glu Ser Asn Thr Lys Leu Lys Asn  
100 105 110

Ile Lys Asn Asn Ile Lys Tyr Lys Asn Ser Phe Asn Ser Ser Tyr Leu  
115 120 125

Val Leu Glu Asp Tyr Lys Ile Ile Thr Asn Glu Val Asn Ile Gln Tyr  
130 135 140

Tyr Tyr Asn Tyr Thr Glu Asp Ser Lys Ile Thr Leu Asn Asn Asn Asp  
145 150 155 160

Leu Val Leu Phe Met Thr Pro Tyr Lys Ile Glu Lys Ile Tyr Ser Lys  
 165 170 175

Asn Ile Phe Ile Asn Gln Tyr Arg Trp Phe Tyr Val Leu Asn Asn Ile  
 180 185 190

Glu Pro Ser Gly Ser Tyr Arg Ile Asn Met Asp Asn Met Gln Lys Ile  
 195 200 205

Lys Thr Tyr Asn Lys Asn Lys Thr Ser Tyr Tyr Cys Lys Asn Pro Lys  
 210 215 220

Leu Leu Phe Ser Asn Tyr Val Lys Ile Asp Lys Ile Pro Ala Ser Arg  
 225 230 235 240

Val Ser Ile Asp Ile Glu Cys Gln His Phe Gly Glu Phe Pro Thr Ala  
 245 250 255

Asn Lys Phe Pro Ile Ser His Ile Cys Ile Asp Trp Tyr Met Asp Lys  
 260 265 270

Asn Thr Asn Pro Ile Lys Lys Ile Ile Thr Leu Ile Asn Tyr Glu Ile  
 275 280 285

Ile Lys Asn Tyr Val Gly Lys Lys Asp Lys Phe Ile Tyr Thr Glu Val  
 290 295 300

Asn Lys Leu Leu Asn Thr Asn Lys Val Tyr Ile Thr Ile Tyr Cys Thr  
 305 310 315 320

Glu Lys Tyr Met Leu His Phe Val Leu Tyr Thr Leu Arg Gln Asp Phe  
 325 330 335

Asp Tyr Val Leu Thr Tyr Asn Gly His Asn Phe Asp Phe Thr Tyr Ile  
 340 345 350

Gln Arg Arg Lys Ile Asn Lys Leu Lys Gly Leu Cys Leu Asp Asn Val  
 355 360 365

Tyr Ser Thr Asn Glu Ile Lys Ile Ser Lys Phe Ser Tyr Asn Gln Asp  
 370 375 380

Thr Thr Tyr Glu Ile Asp Ser Thr Asn Gly Ile Ile Phe Leu Asp Leu

385		390		395		400
Tyr Asn Tyr Ile Lys Lys Thr Tyr Pro Ser Ser Asn Tyr Lys Leu Ser						
	405			410		415
Glu Ile Thr Lys Glu Arg Phe Asn Ile Phe Cys Lys Ile Ser Tyr Asn						
	420		425			430
Asn Asn Glu Tyr Ile Ile Glu Pro Leu Asn Thr Lys Ala Asn Lys Asn						
	435		440			445
Lys Ile Ser Ile Phe Tyr Asp Val Ile Arg Thr Ala Asn Tyr Cys Phe						
	450		455			460
Ile Asn Asn Asn Pro Tyr Lys Lys Asn Lys Thr Glu Ile Ile Asp Asp						
	465		470		475	480
Ile Glu Lys Leu Tyr Asp Leu Thr Ser Ile Lys Asn Ser His Asn Lys						
	485		490			495
Lys Phe Thr Ile Tyr Glu Asn Asp Ile Pro Ile Asn Asp Asn Tyr Ala						
	500		505			510
Thr Val Met Leu Ser Lys Asp Asp Val Asp Ile Gly Asp Lys Asn Ala						
	515		520			525
Tyr Val Phe Thr Lys Glu Lys Ser Asp Asn Ile Ala Tyr Tyr Cys Thr						
	530		535			540
His Asp Thr Val Leu Cys Asn Cys Ile Phe Lys Tyr Asp Met Ile His						
	545		550		555	560
Asp Lys Ile Ile Ala Phe Ser Asn Glu Tyr Leu Leu Pro Gln Cys Met						
	565		570			575
Ala Phe Lys Tyr Lys Ser Ser Asn Asn Ile Ser Gly Leu Leu Lys Thr						
	580		585			590
Leu Tyr Ser Asn Lys Thr Met Ile Tyr Pro Gly Asn Val Glu Phe Glu						
	595		600			605
Lys Phe Glu Gly Gly Tyr Val Ile Glu Pro Lys Gln Lys Tyr Ile Asp						
	610		615			620

Ser Leu Thr Ala Val Phe Asp Phe Asn Ser Glu Tyr Pro Ser Ile Ile  
625 630 635 640

Ile Glu Ala Asn Leu Ser Pro Glu Val Val Lys Val Ile Lys Leu Phe  
645 650 655

Asp Asp Glu Glu Ala Ala Asn Lys Val Glu Lys Tyr Leu Lys Asp Asn  
660 665 670

Tyr Lys Tyr Pro Asp Tyr Cys Tyr Ile Lys Ile Ile Lys Asp Lys Met  
675 680 685

Tyr Lys Phe Ile Leu Met Asp Arg Arg Glu Leu Gly Val Thr Thr Gln  
690 695 700

Met Val Lys Gly Arg Glu Met Lys Asn Met Tyr Lys Asp Leu Lys Asn  
705 710 715 720

Lys Asn Lys Asp Asn Val Asp Leu His Asn Phe Tyr Ser Ser Ala Leu  
725 730 735

Tyr Ser Lys Lys Ile Thr Ile Asn Ser Met Tyr Gly Leu Ser Gly Ser  
740 745 750

Glu Arg Phe Ile Phe Asn Ser Pro Tyr Cys Ala Glu Tyr Cys Val Gln  
755 760 765

Gly Gln Asn Cys Ile Lys Tyr Ile Gln Thr Leu Val Asn Asn Ser Lys  
770 775 780

Tyr Ile Asp Asn Val Leu Ile Leu Asn Lys Cys Asn Asn Pro Phe Thr  
785 790 795 800

Asn Glu Pro Ile Lys Thr Asn Tyr Pro Gly Asn Leu Asn Val Asn Phe  
805 810 815

Thr Phe Asn Val Lys Tyr Gly Asp Thr Ser Leu Phe Ile Thr Val Asn  
820 825 830

Phe Glu Ser Lys Phe Asn Ser Lys Glu Glu Lys Val Lys Val Gly His  
835 840 845

Lys Cys Phe Thr Phe Leu Gly Asn Val Ile Asn Asp Lys Lys Asn Lys  
 850 855 860

Ile Leu Thr Asp Asn Phe Glu Phe Glu Tyr Glu Lys Met Tyr Tyr Trp  
 865 870 875 880

Met Ile Leu Leu Lys Lys Lys Tyr Ile Gly Glu Val Val Ile Asn Met  
 885 890 895

Asp Pro Leu Gln Leu Met Asp Asp Thr Lys Gly Thr Ala Leu Ile Arg  
 900 905 910

Arg Asp Cys Thr Val Ile His Lys Thr Ile Leu Lys Asn Thr Ile Asn  
 915 920 925

Ile Leu Lys Asp Phe Leu Thr Asn Asp Asn Thr Gly Ile Asn Ile Asn  
 930 935 940

Val Lys Ile Asn Asp Tyr Leu Ser Ser Ala Phe Lys Asn Ile Ile Glu  
 945 950 955 960

Asn Ile Gln Asn Leu Asp Ile Asn Asp Phe Lys Lys Ser Val Lys Tyr  
 965 970 975

Ser Gly Val Tyr Lys Asp Pro Asn Tyr Pro Ile Glu Leu Cys Val Lys  
 980 985 990

Glu Tyr Asn Leu Lys Asn Pro Asn Asp Lys Ile Thr Lys Gly Gln Arg  
 995 1000 1005

Phe Asp Phe Ile Tyr Ala His Lys Ile Asn Glu Trp Ser Lys Asp  
 1010 1015 1020

Lys Lys Trp Asn Ile Lys Tyr Thr Ile Asp Ile Ser Lys His Val  
 1025 1030 1035

Ile Ile Leu Glu Asp Tyr Leu Lys Asn Lys Asn Asn Tyr Arg Ile  
 1040 1045 1050

Cys Val Glu Lys Tyr Ile Lys Asp Ile Leu Ser Asn Leu Asp Gln  
 1055 1060 1065

Ile Ile Asn Asp Lys Asn Ile Ile Lys Asn Ile Asp Ile Met Leu  
 1070 1075 1080

Asn Ser Tyr Glu Pro Gln  
 1085

<210> 19

<211> 611

<212> PRT

<213> Amsacta moorei entomopoxvirus

<400> 19

Met Asn Asp Ile Asp Lys Asn Asn Ile Leu Asn Asn Lys Tyr Ile Gly  
 1 5 10 15

Phe His Thr Ile Lys Glu Tyr Leu Asp Lys Tyr Lys Cys Pro Leu Gln  
 20 25 30

Phe Phe Val Gly Ala Pro His Ser Tyr Gln Ser Thr Glu Tyr Leu Asn  
 35 40 45

Lys Ser Tyr Thr Gly Arg Thr Ile Phe Val His Ser Lys Tyr Val Gly  
 50 55 60

Asn Ile Ala Lys Asp Lys Asn Ser Val Ala Leu Arg Asn Ile Lys Lys  
 65 70 75 80

Glu Leu Leu Tyr Leu Gln Asn Met Glu Ile Asn Asn Ser Gly Thr Val  
 85 90 95

Val His Leu Ser Leu Tyr Tyr Asn Lys Asn Gln Glu Glu Ser Leu Lys  
 100 105 110

Tyr Val Ala Asn Glu Leu Asn Lys Phe Cys Lys Val Leu Asp Asn Ile  
 115 120 125

Asp Asn Asn Tyr Phe Asn His Ile Ile Phe Glu Thr Thr Asn Asp Ile  
 130 135 140

Arg His Leu Gly Ala Lys Thr Glu Asp Phe Lys Ile Leu Tyr Asp Asn



145		150		155		160
Leu Asp Ser Asn	Ala Lys Lys Arg Ile	Lys Phe Cys Ile	Asp Thr Ser			
	165		170		175	
His Ile Phe Val	Thr Phe Tyr Asn	Ile Asn Thr Val	Lys Gly Met Ile			
	180		185		190	
Asn Tyr Leu Ala	Lys Phe Asp Leu	Leu Ile Gly Leu	Asp Lys Ile Ile			
	195		200		205	
Leu Ile His Leu	Asn Asp Ser Cys	Gly Leu Pro Leu	Ser Ser Tyr Lys			
	210		215		220	
Pro His Glu Ala	Ile Gly Lys Gly	Asn Ile Phe Lys	Asn Tyr Lys Asp			
	225		230		235	
Asp Leu Ser Ser	Leu His Ile Leu	Lys Thr Tyr Ala	Thr Leu Tyr Asn			
	245		250		255	
Ile Pro Cys Ile	Leu Glu Arg Arg	Asn Glu Val Pro	Asp Gln Ser Ile			
	260		265		270	
Met Asp Glu Met	Lys Ile Tyr Leu	Asp Ile Lys Gln	Asn Met Asn Ile			
	275		280		285	
Asp Asn Phe Met	Ser Met Ile Asn	Lys His Lys Ile	Leu Leu Val Leu			
	290		295		300	
Asn Lys Phe Ala	Asp Ile Tyr Asn	Ile Leu Asn Glu	Ile Lys Tyr Lys			
	305		310		315	
Ala Phe Leu Asn	Ala Ala Tyr Val	Ile Gln Asn Thr	Pro Val Ile Ile			
	325		330		335	
Phe Lys Tyr Lys	Asn Val Asn Asn	Lys Phe Ile Leu	Asn Glu Ser Lys			
	340		345		350	
Glu Asn Ile Ile	Gln Lys Tyr Lys	Asn Leu Lys Ser	Ile Gly Thr Ser			
	355		360		365	
Ile Ser Asp Ile	Ile Tyr Glu Leu	Leu Ser Thr Asn	Lys Val Glu Lys			
	370		375		380	

Leu Ile Asn Leu Glu Asn Asn Ser Ser Tyr Lys Tyr Ile Lys Ile Leu  
 385 390 395 400

Thr Ser Ile Leu Phe Ile Gly Pro Lys Lys Ala Gln Ser Leu Leu Lys  
 405 410 415

Leu Asn Ile Lys Asn Ile Asn Asp Leu Ile Glu Lys Lys Asp Asn Ile  
 420 425 430

Ile Asn Met Gly Ile Leu Thr Ile His Glu Ile Lys Ile Ile Glu Tyr  
 435 440 445

Ile Lys Asp Met Glu Pro Val Ser Arg Asn Phe Ile Asn Asp Leu Lys  
 450 455 460

Gln Asn Ile Asn Leu Ser Ser Glu Cys Glu Trp Tyr Ile Leu Gly Ser  
 465 470 475 480

Tyr Ala Arg Gly Leu Asp Tyr Ser Lys Asp Ile Asp Ile Leu Ile Ile  
 485 490 495

Asp Phe Thr Ile Asp Lys Phe Leu Glu Glu Leu Lys Lys Ile Ala Lys  
 500 505 510

Leu Met Tyr Ile Ile Arg Lys Gly Asn Asn Ile Phe Ser Gly Val Phe  
 515 520 525

Leu Trp Gln Gly Lys Lys Phe Ile Leu Glu Ile Asn Lys Val Asn Asn  
 530 535 540

Lys Glu Lys Tyr Thr Ala Ile Met His Phe Thr Gly Ser Lys Lys Phe  
 545 550 555 560

Asn Ile Phe Met Arg Asn Ile Ala Lys Ser Glu Asn Met Ile Leu Asn  
 565 570 575

Gln Tyr Ser Leu Lys Lys Asp Asn Val Glu Leu Pro Ile Thr Lys Glu  
 580 585 590

Glu Asp Ile Phe Asp Tyr Leu Lys Ile Lys Tyr Ile Pro Asn Asn Lys  
 595 600 605

Arg Asn Ile  
610

<210> 20

<211> 1381

<212> PRT

<213> Amsacta moorei entomopoxvirus

<400> 20

Met Tyr Phe Asn Ile Leu Asn Gly Leu Leu Trp Lys Tyr Tyr Ile Ile  
1 5 10 15

Lys Arg Lys Lys Tyr Ile Tyr Asp Met Leu Glu Tyr Leu Leu Leu Ile  
20 25 30

Leu Phe Phe Thr Leu Leu Tyr Ser Phe Lys Lys Asn Ile Lys Tyr Tyr  
35 40 45

Asp Asn Asp Leu Asn Asn Ile Asn Lys Ile Asn Asn Asn Thr Asn Ile  
50 55 60

Ile Tyr Tyr Pro Lys Ser Asn Ile Ser Ile Lys Ile Ile Glu Asn Val  
65 70 75 80

Ala Lys Glu Leu Lys Ile Asn Lys Tyr Tyr Gly Ser Ser Asn Glu Asn  
85 90 95

Glu Ile Ile Asn Phe Ile Asp Thr Asn Glu Thr Ile Phe Ile Leu Phe  
100 105 110

Asn Asn Thr Cys Glu Asn Leu Leu Tyr Thr Ile Arg Phe Asn Asn Asn  
115 120 125

Glu Asn Asn Asp Arg Leu Leu Ile Asn Ile Gln Trp Leu Ile Asn Met  
130 135 140

Asn Tyr Leu Arg Leu Leu Ser Asn Lys Asn Ile Asn Ile Asp Ile Asp  
145 150 155 160

Ile Asn Glu Tyr Ile Tyr Lys Asn Phe Asn Thr Asn Ile Leu Phe Tyr  
 165 170 175

Thr Tyr Tyr Ser Ile Leu Ile Ile Ala Phe Ile Ser Phe Ile Leu Lys  
 180 185 190

Asn Asn Asn Asp Asn Asn Asp Pro Met Phe Lys Ile Ile Lys Val Pro  
 195 200 205

Lys Ile Leu Ile Tyr Ile Ser Asn Phe Ile Cys Ser Ile Pro Phe Gly  
 210 215 220

Ile Ile Tyr Ser Val Phe Gly Thr Ile Ile Leu Thr Ile Ser Glu Asp  
 225 230 235 240

Pro Leu Ile Asn Asn Asn Asn Asn Ile Ile Met Phe Leu Ile Leu Leu  
 245 250 255

Ile Tyr Phe Ile Ser Val Ile Ser Met Ala Tyr Leu Asn Phe Phe Ile  
 260 265 270

Leu Leu Ile Tyr Lys Tyr Lys Ile Phe Val Ile Met Cys Val Tyr Val  
 275 280 285

Leu Thr Ile Ile Pro Ile Thr Leu Tyr Asn Asn Leu Asn Ser Asp Ile  
 290 295 300

Asn Ile Phe Ile Gly Leu Ile Pro His Ile Pro Leu Tyr Trp Ile Phe  
 305 310 315 320

Asp Gln Leu Asn Tyr Val Glu Lys Gln Asn Lys Ser Leu Thr Phe Asn  
 325 330 335

Asn Asn Ile Ser Tyr Ser Ile Tyr Ser Lys Ser Ile Leu Ile Ser Ile  
 340 345 350

Ile Tyr Leu Ile Leu Gln Ser Phe Ile Tyr Ile Ser Ile Ile His Ile  
 355 360 365

Ile Lys Leu Ile Tyr Lys Ile Cys Lys Lys Tyr Met Lys Met Lys Tyr  
 370 375 380

Ile Tyr Ile Ile Asn Glu Asn Asn Asn Tyr Met Leu Glu Thr Glu Asn

385		390		395		400
Asn Asp Tyr Tyr	Val Lys Ile Gln Asn Ile Tyr Lys Tyr Tyr	Asp Asn				
	405		410		415	
Asn Phe Ile Leu	Asn Asn Ile Cys Leu Asp Ile Ile Lys Asn Asn Thr					
	420		425		430	
Thr Val Leu Leu Gly	Asn Asn Ser Ala Gly Lys Ser Thr Leu Leu Ser					
	435		440		445	
Ile Ile Phe Gly Leu Ile Lys Pro Asn Lys Gly Lys Ile Leu Thr Asn						
	450		455		460	
Asn Ile Lys Ile Gly Tyr Cys Pro Gln Asn Asn Ile Phe Thr Asp Phe						
	465		470		475	
Thr Val Lys Glu Asn Ile Tyr Leu Phe Asn Ile Leu Arg Gly Leu Ser						
	485		490		495	
Ser Leu Gln Ser Lys Ile Lys Thr Asn Glu Ile Ile Ile Tyr Leu Lys						
	500		505		510	
Leu His Asp Ile Glu Asn Cys Ile Ile Thr Glu Leu Ser Glu Cys Ser						
	515		520		525	
Lys Arg Lys Leu Gln Leu Ala Phe Ser Leu Ile Asp Asp Ser Asp Phe						
	530		535		540	
Ile Leu Ile Asp Glu Pro Thr His Asn Ile Asp Leu Lys Ser Lys Gln						
	545		550		555	
Glu Ile Trp Asp Leu Ile Ser Leu Leu Lys Arg Asn Lys Thr Ile Leu						
	565		570		575	
Ile Thr Thr His Cys Ile Asp Glu Val Glu Leu Leu Ala Asp Asn Leu						
	580		585		590	
Ile Ile Leu Asn Asn Gly Asn Val Lys Tyr Asn Ser Thr Leu Phe Asn						
	595		600		605	
Ile Lys Lys Asp Ala Asn Val Thr Tyr Lys Leu Ser Ile His Asn Asn						
	610		615		620	

Ser Thr Asp Asp Lys Ile Lys Asn Ile Ile Ile Asn Ser Gly Phe Ile  
625 630 635 640

Ile Leu Asn Ile Asn Lys Ile Asp Glu Asn Asn Ser Ile Tyr Asn Ile  
645 650 655

Tyr Lys Thr Glu Asn Ser Asn Phe Leu Lys Leu Phe Glu Leu Leu Glu  
660 665 670

Asn Val Asn Cys Asp Ile Ile Tyr Phe Lys Ser Asn Thr Leu Asn Asp  
675 680 685

Ile Leu Tyr Lys Leu Cys Ser Glu Asp Ile Ile Ile Pro Asp Asp Ser  
690 695 700

Tyr Ile Asn Asn Leu Asn Tyr Asn Asp Met Phe Ile Ser Glu Ile Met  
705 710 715 720

Gly Phe Asn Lys Ile Met Arg Gln Phe Ile Glu Leu Phe Lys Arg Asn  
725 730 735

Ile Tyr Tyr Ile Arg Lys Asn Ile Leu Leu Phe Val Ile Ile Asn Phe  
740 745 750

Ile Leu Ser Ile Leu Ile Val Tyr Val Gly Ile Val Tyr Ile Lys Lys  
755 760 765

Tyr Glu Asn Leu Tyr Leu Tyr Asn Phe Val Ile Ile Asn His Asn Ile  
770 775 780

Asp Asn Phe Ile Asn Asn Ser Asn Tyr Leu Leu Asp Ile Lys His Asn  
785 790 795 800

Ser Thr Tyr Asn Lys Ile Thr Tyr Ile Pro Leu Phe Lys Tyr Ser Gly  
805 810 815

Ser Ile Ala Ile Asn Ile Ile Ser Asn Ile Ile Ala Lys Ile Asn Ile  
820 825 830

Pro Asn Ile Glu Lys Asp Ile Ile Thr Thr Ile Phe Tyr Pro Met Tyr  
835 840 845

Gln Asn Lys Thr Ser Ile Leu Thr Asn Leu Phe Ile Ser Ile Ile Leu  
850 855 860

Gln Leu Tyr Cys Ile Asn Tyr Asn Lys Leu Ile Lys Lys Asp Asn Ile  
865 870 875 880

Asn Lys Thr Arg Lys Gln His Ile Ile Asn Gly Cys Asn Pro Glu Leu  
885 890 895

His Trp Ile Thr Thr Leu Leu Phe Asn Met Ile Leu Phe Ser Ile Ser  
900 905 910

Val Ile Pro Ile Ile Leu Tyr Met Leu Asn Ile Lys Ser Phe Phe Asp  
915 920 925

Leu Ile Ile Leu Tyr Phe Ile Leu Ile Ile Asn Ala Leu Ser Phe Met  
930 935 940

Leu Phe Ser Ile Ile Ile Leu Met Phe Asp Asn Gln Ser Asp Lys Ile  
945 950 955 960

Ile Leu Ile Leu Val Phe Ile Leu Gly Ile Leu Leu Pro Ile Tyr Lys  
965 970 975

Ile Lys Tyr Lys Asn Ile Ile Leu Asp Ile Leu Ser Tyr Ile Phe Ile  
980 985 990

Pro Ser Cys Ile Ser Met Ser Ile Ile Glu Tyr Leu Asn Thr His Lys  
995 1000 1005

Leu Asn Tyr Ile Ile Ser Ile Ile Ile Gln Ile Leu Leu Tyr Leu  
1010 1015 1020

Ile Leu Ile Ile Leu Ile Glu Arg Gly Leu Ile Asp Ile Ile Tyr  
1025 1030 1035

Asn Lys Ile Ile Asn Leu Lys Tyr Asn Arg Lys Asn Asn Asn Tyr  
1040 1045 1050

Phe Glu Leu Gln Asn Ile Asn Lys Tyr Thr Asp Tyr Asn Ser Ser  
1055 1060 1065

Leu Ile Met Ser Asn Val Tyr Lys Ile Tyr Asn Asn Lys Leu Ala  
 1070 1075 1080

Leu Asn Asn Ile Asn Phe Lys Ile Ser Glu Gly Lys Cys Phe Gly  
 1085 1090 1095

Ile Ile Gly Gly Asn Gly Cys Gly Lys Ser Thr Ile Phe Lys Ile  
 1100 1105 1110

Leu Ser Gly Glu Glu Cys Val Thr Lys Gly Asn Ile Tyr Ile Gly  
 1115 1120 1125

Cys Ser Asn Arg Ser Trp Ile Leu Lys Ser Asn Tyr Phe Lys Lys  
 1130 1135 1140

Ile Ser Tyr Cys Ser Gln Phe Phe Gly Ile Asp Thr Phe Leu Thr  
 1145 1150 1155

Gly Arg Gln Asn Leu Lys Leu Ile Met Ile Leu Asn Gly Phe Ser  
 1160 1165 1170

Asp Lys His Ile Gln Tyr Tyr Ile Asn Ile Trp Leu Lys Leu Leu  
 1175 1180 1185

Asn Ile Glu Lys Tyr Ala Asp Lys Ala Val Tyr Thr Tyr Ser Thr  
 1190 1195 1200

Gly Ile Ile Lys Arg Leu Lys Ile Ala Met Ser Leu Ala Pro Arg  
 1205 1210 1215

Ser Ile Leu Thr Leu Met Asp Glu Pro Thr Ser Gly Ile Asp Ile  
 1220 1225 1230

Val Ser Lys Gln Ile Ile Trp Lys Thr Ile Lys Tyr Ile Ile Asn  
 1235 1240 1245

Tyr Asn Tyr Tyr Asn Tyr Tyr Lys His Ser Ile Leu Ile Ser Ser  
 1250 1255 1260

Asn Asn Ile Glu Glu Ile Glu Tyr Leu Cys Ser Asn Val Ile Ile  
 1265 1270 1275

Leu Asp Ser Gly Asn Ile Met Tyr Asn Asp Thr Leu Glu Asn Ile



1280	1285	1290
Lys Asn Ile His Ser Thr	Lys Ile Ile Asn Ile	Lys Leu Leu His
1295	1300	1305
Tyr Asp Asn Asn Lys Ile	Cys Lys Ile Lys Asn	Lys Leu Lys Asn
1310	1315	1320
Lys Gly Phe Met Leu Lys	Ser Asp Asn Lys Phe	Lys Leu Thr Phe
1325	1330	1335
Cys Val Ser Lys Asn Ile	Asn Leu Lys Tyr Ser	Glu Leu Phe Lys
1340	1345	1350
Ile Leu Tyr Ile Leu Lys	Asn Asn Tyr Ser Asp	Ile Ile Asp Gln
1355	1360	1365
Tyr Asp Ile Ser Asp Thr	Asn Ile Glu Gln Leu	Phe Ser
1370	1375	1380

<210> 21

<211> 79

<212> PRT

<213> Amsacta moorei entomopoxvirus

<400> 21

Met Asn Tyr Tyr Ile Leu Leu Cys Leu Phe Met Leu Phe Ser Ser Ser
1 5 10 15
Tyr Asn Phe Lys Leu Ile Asn Asn Asn Ile Cys Asn Glu Asp Tyr Asp
20 25 30
Pro Gly Ile Cys Arg Ile Gly Asp Ile Arg Trp Tyr Tyr Asn Tyr Asn
35 40 45
Ile Lys Asp Cys Lys Ile Phe Ile Tyr Gly Gly Cys Gly Gly Asn Met
50 55 60
Asn Asn Phe Asn Asn Tyr Glu Asp Cys Ile Asn Lys Cys Leu Ile
65 70 75

&lt;210&gt; 22

&lt;211&gt; 572

&lt;212&gt; PRT

&lt;213&gt; Amsacta moorei entomopoxvirus

&lt;400&gt; 22

Met Asn Ile Tyr Leu Lys Asn Ala Ser Asn Asp Thr Ile Ser His Leu  
1 5 10 15

Ser Lys Phe Thr Asn Gln Ile Asn Asp Ile Ile Ser Phe Asp Ile Asn  
20 25 30

Asn Phe Thr Lys Asn Val Leu Ile Met Arg Asn Asn Ile Asn Asn Ile  
35 40 45

Arg Thr Asn Phe Glu Asn Val Ser Asp Asp Asn Ser Ile Lys Arg Arg  
50 55 60

Ile Thr Glu Phe Phe Asp Lys Gln Asn Thr Pro Asn Leu Lys Leu Gly  
65 70 75 80

Ser Ile Ile Ser Ile Ile Lys Phe Gln His Leu Thr Val Thr Tyr Val  
85 90 95

Asn Lys Ile Ile Lys Glu Ile Val Thr Tyr Lys Cys Asn Thr Arg Glu  
100 105 110

Ile Asn Ile Val Asn Phe Ser Ser Val Thr Ser Gln Ile Ser Asn Tyr  
115 120 125

Asp Asn Pro Ile Leu Asn Glu Ile Leu Lys Gln Tyr Val Tyr Lys Gln  
130 135 140

Lys Leu Lys Asn Val Thr Val Asn Asn Asp Lys Lys Lys Ile Ile Asp  
145 150 155 160

Pro Asp Asp Glu Lys Leu Ala Glu Ser Ile Lys Lys Ile Leu Glu Glu  
165 170 175

Ile Leu Lys Ile Leu Leu Ile Ile Lys Asn Asn Asp Cys Val Ala Tyr  
 180 185 190

Gly Ser Phe Thr Cys Tyr Asn Ile Asn Arg Ser Ile Lys Tyr Asn Asp  
 195 200 205

Ile Asp Leu Tyr Ser Thr Asp Ala Tyr Arg Ile Leu Ile Phe Phe Met  
 210 215 220

Ile Tyr Ile His Leu Thr Ile Gly His Asp Thr Cys Leu Phe Ser Ile  
 225 230 235 240

Pro Phe Ile Thr Gly His Ile Ser Leu Lys Tyr Lys Asn Ile Phe Ile  
 245 250 255

Ile Asp Cys Ile Phe Leu Asp Asn Ser Ile Ile Asn Val Ile Asn Lys  
 260 265 270

Ser Leu Ile Asn Asn Ile Tyr Phe Ile Asp Pro Gly Leu Gln Met Leu  
 275 280 285

Asn Asn Phe Arg Met Leu Ser Glu Asn Phe Arg Ser Tyr Lys Ile Tyr  
 290 295 300

Glu Lys Met Glu Glu Ser Leu Asn Lys Tyr Lys Thr Leu Leu Asn Tyr  
 305 310 315 320

Phe Val Asn Asn Asn Asn Lys Phe Asn Lys Gln Arg Leu Asn Tyr Trp  
 325 330 335

Leu Lys Ser Asp Val Cys Arg Asn Asn Phe Pro Tyr Thr Ile Val Asp  
 340 345 350

Asn Thr Ile Leu Ile Ser Ile Lys Glu Leu Ile Asp Ile Ser Pro Tyr  
 355 360 365

Asp Tyr Ile Met Ile Val Leu Asp Ser Pro Ser Asp Ile Met Glu Lys  
 370 375 380

Leu Ser Asn Ile Ser Gly Leu Phe Ser Arg Lys Tyr Gly Ala Phe Leu  
 385 390 395 400

Asn Glu Ile Phe Phe Glu Thr Lys Lys Ile Lys Asn Lys Ile Asn Thr  
 405 410 415

Tyr Ala Gly Asn Thr Asn Asn Ile Thr Gln Leu Ile Asp Glu Asn Lys  
 420 425 430

Leu Ile Lys Leu Asn Arg Ser Asp Ile Asn Met Pro Tyr Asn Ile Asn  
 435 440 445

Pro Asn Lys Lys Tyr Leu Ile Phe Ser Asn Leu Thr Thr Ser Thr Tyr  
 450 455 460

Val Tyr Phe Glu Asn Asp Lys Met Thr Asp Ile Ser Val Lys Asn Leu  
 465 470 475 480

Ile Ser Phe Ile Ser Thr Ala Cys Leu Tyr Asn Leu Leu His Lys Lys  
 485 490 495

Asp Asp Phe Gly Met Glu Leu Tyr Tyr Leu Thr Leu His Cys Leu Thr  
 500 505 510

Phe Thr Glu Thr Arg Lys Leu Asn Glu Tyr Lys Val Ile Asp Arg Tyr  
 515 520 525

Lys Ile Gly Glu His Lys Glu Ile Ser Leu Cys Lys Asn Leu Phe Asn  
 530 535 540

Ser Ile Tyr Lys Asn Lys Ser Met Glu Asp Glu Tyr Met Asp Tyr Asn  
 545 550 555 560

Thr Phe Ile Asp Leu Thr Asn Ile Asn Gly Gly Tyr  
 565 570

<210> 23

<211> 50000

<212> DNA

<213> Amsacta moorei entomopoxvirus

<400> 23

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aaatatttag aatttattga aaattagtaa aattagattg ttctaaaaca tatattgatt	180
ctctaaaagg aatacattat cttactaatt tacaaaaatt aattctttta aagaaatatg	240
ttgccttaat aatattaaaa aaataaattg ttcatataca atcattgatt ctctaaaagg	300
aataagtctt aataatttag aagaattata ttgttataat ataaaaattt attcttttaa	360
tataataata aaaaatctgc ttattaaaaa tattaaatgg ttataaatat ataaattaat	420
tattttatat aaattattgt taaacattta tattaatatt ctaatattaa aaattgaaaa	480
aaaaaataat tatgttaaaa tggagttacc tgtagaaatg ttagaaatta tatttaatta	540
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attaatatat aataattatt atataaaatc tttagaaggt attgaaaatt ttactaaatt	720
aataaaatta tattgttaca atacaagaat cgattcttta aaaggaatag aaaatctcat	780
taaattaaaa gaattatatt gttttaatac aaatattaat tcttttagtat atttaaaaaa	840
tcttattaat ttaacagaat tatattgttt tgaaacaaat atttattctt taaaaggaat	900
agaaaatctc attaatTTaa aagaatttga ttgttcttat acactaatag attcttttaa	960
agagataaaa aatcttatta atttacaaaa attaaattgc tcacatacaa ttatttattc	1020
tctcgaagga atagaaaatc tcattaattt agaaaaacta gattgttctt atacaagtat	1080
taattcttta aaagaaataa aaaatcttat taatttaaaa aaattagaat gttatgaaac	1140
aaatatttat tctcttaaag agttacaaaa tctaattaat ttaaaaaaat tagattgttc	1200
ttatacaaaa attaatctt taaaagaatt acaaaatctt attaatTTaa aaaaattaga	1260
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taattcttta aaaggatatg aaaatcttat taatttagaa atattatatt gtaataatac	1800

aaatattatt tctttagaag gaataaaaaa tcttattaaa ttagaagaat tatattattt	1860
taatacaaat attattttatt aataagttta ttattttattt atagtatata cattaatatt	1920
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atacaaaaata ctaatgagat tttagaaaaa attcttaata ttttaactga attaaaaaca	2040
gaaattaata gaaaaaatga tgatgaatat tctgatttat atgattcaga ataattaata	2100
agaatcatat tctatacaac aatcacaca ccatgcttca aagatagaaa atccacaata	2160
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tctatcataa tctataatat ctgttatatt catattatat aaagaagtta ttctacttct	3480

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<210> 28

<211> 501

<212> DNA

<213> Amsacta moorei entomopoxvirus

&lt;220&gt;

&lt;221&gt; exon

&lt;222&gt; (1)..(501)

&lt;223&gt;

&lt;400&gt; 28

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Met Asn Lys Ile Gln Val Ile Gly Phe Asn Asn Leu Thr Leu Leu Asn	
1 5 10 15	
ata caa att tta tct att aat aaa aaa act tat gca aaa att aca act	96
Ile Gln Ile Leu Ser Ile Asn Lys Lys Thr Tyr Ala Lys Ile Thr Thr	
20 25 30	
ata gaa aat aat aga cct cat tgg gtg ttt gat tta tat ttt tat ata	144
Ile Glu Asn Asn Arg Pro His Trp Val Phe Asp Leu Tyr Phe Tyr Ile	
35 40 45	
aaa ata aca cgt ttt ttt aga aca ata tac gaa tat agt ata tat ggt	192
Lys Ile Thr Arg Phe Phe Arg Thr Ile Tyr Glu Tyr Ser Ile Tyr Gly	
50 55 60	
act gtt cca ata gaa aat aac gaa aga tat ata aga ata tat aat aat	240
Thr Val Pro Ile Glu Asn Asn Glu Arg Tyr Ile Arg Ile Tyr Asn Asn	
65 70 75 80	
act aca ttt aaa tta ttt cat gct gaa cca ctt ggg aga tta tta att	288
Thr Thr Phe Lys Leu Phe His Ala Glu Pro Leu Gly Arg Leu Leu Ile	
85 90 95	
tat gat aaa aat ggt gaa tta tta ttt cct att aac gtt ata tat att	336
Tyr Asp Lys Asn Gly Glu Leu Leu Phe Pro Ile Asn Val Ile Tyr Ile	
100 105 110	
tgg aat tta gat tct tta aaa ata gtt gat tat gct ata cta aca tta	384
Trp Asn Leu Asp Ser Leu Lys Ile Val Asp Tyr Ala Ile Leu Thr Leu	
115 120 125	
aat aat ata tat aat tta ttt ttg tat ttt gtt ata ttt ata atg ttt	432
Asn Asn Ile Tyr Asn Leu Phe Leu Tyr Phe Val Ile Phe Ile Met Phe	
130 135 140	
ata ata tat tat tta tat att tat ata aat aat agg aaa gat gtt ttg	480
Ile Ile Tyr Tyr Leu Tyr Ile Tyr Ile Asn Asn Arg Lys Asp Val Leu	
145 150 155 160	
aaa aaa aat aat ata cat taa	501
Lys Lys Asn Asn Ile His	
165	

&lt;210&gt; 29

&lt;211&gt; 432

&lt;212&gt; DNA

&lt;213&gt; Amsacta moorei entomopoxvirus

&lt;220&gt;

&lt;221&gt; exon

&lt;222&gt; (1)..(432)

&lt;223&gt;

&lt;400&gt; 29

atg gaa cca ata ttt aaa tat atg ttt gtt aca gaa aat gct ttt gaa	48
Met Glu Pro Ile Phe Lys Tyr Met Phe Val Thr Glu Asn Ala Phe Glu	
1 5 10 15	

cct att aga cag aca tca aaa tct gca gga atg gat tta aaa agt gca	96
Pro Ile Arg Gln Thr Ser Lys Ser Ala Gly Met Asp Leu Lys Ser Ala	
20 25 30	

tat gat tat att gtt tca gca cat gat aaa aaa tta ata aaa act gat	144
Tyr Asp Tyr Ile Val Ser Ala His Asp Lys Lys Leu Ile Lys Thr Asp	
35 40 45	

tta att ata gaa att cct aaa gga tgt tat gca aga tta gct ccc aga	192
Leu Ile Ile Glu Ile Pro Lys Gly Cys Tyr Ala Arg Leu Ala Pro Arg	
50 55 60	

tct gat tta gct cta aat aaa ttt att gat att gga gct gga gta att	240
Ser Asp Leu Ala Leu Asn Lys Phe Ile Asp Ile Gly Ala Gly Val Ile	
65 70 75 80	

gac gaa gat tat aga gga aat gtg gga gta ata tta ttt aat cat tct	288
Asp Glu Asp Tyr Arg Gly Asn Val Gly Val Ile Leu Phe Asn His Ser	
85 90 95	

aat gaa gat ttt ata ata aat aga gga gat aga ata tct caa tta ata	336
Asn Glu Asp Phe Ile Ile Asn Arg Gly Asp Arg Ile Ser Gln Leu Ile	
100 105 110	

tgt gaa aaa att tta tat cct aaa atg tta aaa gtc gat agt tta tca	384
Cys Glu Lys Ile Leu Tyr Pro Lys Met Leu Lys Val Asp Ser Leu Ser	
115 120 125	

gaa aca aaa aga tct gat ttt ggt ttt gga tct act ggt tat aat taa	432
Glu Thr Lys Arg Ser Asp Phe Gly Phe Gly Ser Thr Gly Tyr Asn	
130 135 140	

&lt;210&gt; 30

&lt;211&gt; 780

&lt;212&gt; DNA

&lt;213&gt; Amsacta moorei entomopoxvirus

&lt;220&gt;

&lt;221&gt; exon

&lt;222&gt; (1)..(780)

&lt;223&gt;

&lt;400&gt; 30

atg ttt aaa aca gat tta act aat gaa gaa gta tca gaa gct gct aat	48
Met Phe Lys Thr Asp Leu Thr Asn Glu Glu Val Ser Glu Ala Ala Asn	
1 5 10 15	

aaa tta ata aaa aat aat act tgt aat ttc tat gaa tta aaa tta gaa	96
Lys Leu Ile Lys Asn Asn Thr Cys Asn Phe Tyr Glu Leu Lys Leu Glu	
20 25 30	

aat att tta gac aat att gat tta aca aat aat tgt ata tat tgt aat	144
Asn Ile Leu Asp Asn Ile Asp Leu Thr Asn Asn Cys Ile Tyr Cys Asn	
35 40 45	

gat gta att aaa gat aaa att att ata gat aca aac aat ata aaa gtg	192
Asp Val Ile Lys Asp Lys Ile Ile Ile Asp Thr Asn Asn Ile Lys Val	
50 55 60	

gga tat ttt tgt aca ata aca tgc aaa cac ata tat tat tca ata ata	240
Gly Tyr Phe Cys Thr Ile Thr Cys Lys His Ile Tyr Tyr Ser Ile Ile	
65 70 75 80	

aga aca att ttc aat tta ccc att cat aaa att att aat ttt ata cca	288
Arg Thr Ile Phe Asn Leu Pro Ile His Lys Ile Ile Asn Phe Ile Pro	
85 90 95	

ttt ttt tta tta tcc gaa gaa tct aaa att aaa tat aaa aat ata aaa	336
Phe Phe Leu Leu Ser Glu Glu Ser Lys Ile Lys Tyr Lys Asn Ile Lys	
100 105 110	

aat att att aat tat tat aat tat gat gat ata tct att ttt agt aaa	384
Asn Ile Ile Asn Tyr Tyr Asn Tyr Asp Asp Ile Ser Ile Phe Ser Lys	
115 120 125	

tat aaa gat aat aat aat ata tat act gaa ttt aaa tta tta att aat	432
Tyr Lys Asp Asn Asn Asn Ile Tyr Thr Glu Phe Lys Leu Leu Ile Asn	
130 135 140	



aat aaa ttt att tat ctc caa gaa tcg ttt gaa tat ata tca aaa agt	480
Asn Lys Phe Ile Tyr Leu Gln Glu Ser Phe Glu Tyr Ile Ser Lys Ser	
145 150 155 160	
aat aat tgt ata tat tgt tat tct act aat ata aat gat aaa ata ata	528
Asn Asn Cys Ile Tyr Cys Tyr Ser Thr Asn Ile Asn Asp Lys Ile Ile	
165 170 175	
tta gag cat aat aat gga att att aaa ggt ttt tgt tct ata gtt tgt	576
Leu Glu His Asn Asn Gly Ile Ile Lys Gly Phe Cys Ser Ile Val Cys	
180 185 190	
aga gat tcg ata tct aaa caa ata tat aat aca att atg cct att tat	624
Arg Asp Ser Ile Ser Lys Gln Ile Tyr Asn Thr Ile Met Pro Ile Tyr	
195 200 205	
aaa ttt agt gca tat ttg gta cca ttt gaa tta ata aaa aat aaa aaa	672
Lys Phe Ser Ala Tyr Leu Val Pro Phe Glu Leu Ile Lys Asn Lys Lys	
210 215 220	
gaa ttt tta aat aat att aat cat ata aaa aat att gat aat tta tat	720
Glu Phe Leu Asn Asn Ile Asn His Ile Lys Asn Ile Asp Asn Leu Tyr	
225 230 235 240	
ggt ggt tat tgt cat tta act aat aat aaa act aaa gta gaa tta ttt	768
Gly Gly Tyr Cys His Leu Thr Asn Asn Lys Thr Lys Val Glu Leu Phe	
245 250 255	
att aca aat taa	780
Ile Thr Asn	

&lt;210&gt; 31

&lt;211&gt; 1050

&lt;212&gt; DNA

&lt;213&gt; Amsacta moorei entomopoxvirus

&lt;220&gt;

&lt;221&gt; exon

&lt;222&gt; (1)..(1050)

&lt;223&gt;

&lt;400&gt; 31

atg gtt ttc gaa cat aag ata ttt tca tat aat ttt act gat att aaa	48
Met Val Phe Glu His Lys Ile Phe Ser Tyr Asn Phe Thr Asp Ile Lys	

1	5	10	15	
aaa aaa aaa ata tat cca ata tgc aat tgt att att aat att ttt gat				96
Lys Lys Lys Ile Tyr Pro Ile Cys Asn Cys Ile Ile Asn Ile Phe Asp				
20		25	30	
aaa gaa att aaa ata cca act tta act aaa gca ata ata gac acc aaa				144
Lys Glu Ile Lys Ile Pro Thr Leu Thr Lys Ala Ile Ile Asp Thr Lys				
35		40	45	
cat aat tta gga cct ata tat cta aat ata gct aat atg ctg gcg tat				192
His Asn Leu Gly Pro Ile Tyr Leu Asn Ile Ala Asn Met Leu Ala Tyr				
50		55	60	
gtt gat ata ata tat tta ttt aat aat aat tta gat gaa ata aat aat				240
Val Asp Ile Ile Tyr Leu Phe Asn Asn Asn Leu Asp Glu Ile Asn Asn				
65		70	75	80
tgt ggt ata tac tta ccg att att gac gat ggt agc aaa cat ttt tta				288
Cys Gly Ile Tyr Leu Pro Ile Ile Asp Asp Gly Ser Lys His Phe Leu				
85		90	95	
act tat aaa gat ata aaa tta ttt ata ttt gat gac gaa act ggt aaa				336
Thr Tyr Lys Asp Ile Lys Leu Phe Ile Phe Asp Asp Glu Thr Gly Lys				
100		105	110	
ata aaa att att gat aat cct aaa cat tct gat aaa cat cat ata ata				384
Ile Lys Ile Ile Asp Asn Pro Lys His Ser Asp Lys His His Ile Ile				
115		120	125	
aat tta tct aaa gaa cgt aaa aca gat gat gct ata ggt tca tca cac				432
Asn Leu Ser Lys Glu Arg Lys Thr Asp Asp Ala Ile Gly Ser Ser His				
130		135	140	
gtt tta tta ttt tca tgt aat tca aaa att gaa gaa aat atc aat ttg				480
Val Leu Leu Phe Ser Cys Asn Ser Lys Ile Glu Glu Asn Ile Asn Leu				
145		150	155	160
cat aaa aat att tta tta aca ttt aaa gat tat cct gtg aaa gtt gat				528
His Lys Asn Ile Leu Leu Thr Phe Lys Asp Tyr Pro Val Lys Val Asp				
165		170	175	
ata aaa aat gaa ata gaa aat tct aaa cat tat tat gaa aaa aat tta				576
Ile Lys Asn Glu Ile Glu Asn Ser Lys His Tyr Tyr Glu Lys Asn Leu				
180		185	190	
tta tat aaa aaa cca ttt tct atg tat agc aaa tat cat gaa gaa aaa				624
Leu Tyr Lys Lys Pro Phe Ser Met Tyr Ser Lys Tyr His Glu Glu Lys				
195		200	205	
gat att tat act ata gat ata aga tat aat cat tat gat gat att cct				672
Asp Ile Tyr Thr Ile Asp Ile Arg Tyr Asn His Tyr Asp Asp Ile Pro				
210		215	220	
aaa gaa aat ata aaa aaa ttc ttt att gat ata ttt aat aaa ata gca				720
Lys Glu Asn Ile Lys Lys Phe Phe Ile Asp Ile Phe Asn Lys Ile Ala				
225		230	235	240

gat ata ttt gaa aat att aaa att aaa aat aat gtt gat tat agt 768  
 Asp Ile Phe Glu Asn Ile Lys Ile Lys Lys Asn Asn Val Asp Tyr Ser  
 245 250 255

aat aaa ata agt tat tct aat ata tta gat cat aaa atg aat tat aaa 816  
 Asn Lys Ile Ser Tyr Ser Asn Ile Leu Asp His Lys Met Asn Tyr Lys  
 260 265 270

tat att aac gta gat gat att ata gaa aag aat aaa atg gat gca ttg 864  
 Tyr Ile Asn Val Asp Asp Ile Ile Glu Lys Asn Lys Met Asp Ala Leu  
 275 280 285

tgt tct ata aat gat ata cct gga ata aat gga aca tat tta aaa cca 912  
 Cys Ser Ile Asn Asp Ile Pro Gly Ile Asn Gly Thr Tyr Leu Lys Pro  
 290 295 300

tca gat gaa gag att aat gac gca gaa tat tca tta aat act att atg 960  
 Ser Asp Glu Glu Ile Asn Asp Ala Glu Tyr Ser Leu Asn Thr Ile Met  
 305 310 315 320

aga aat aca ata aaa gaa tta tta gaa tct ttt ata aat ttt att gat 1008  
 Arg Asn Thr Ile Lys Glu Leu Leu Glu Ser Phe Ile Asn Phe Ile Asp  
 325 330 335

gaa aca tac gaa gaa cgt tta aat agt aaa aat ata tat taa 1050  
 Glu Thr Tyr Glu Glu Arg Leu Asn Ser Lys Asn Ile Tyr  
 340 345

<210> 32

<211> 2469

<212> DNA

<213> Amsacta moorei entomopoxvirus

<220>

<221> exon

<222> (1) .. (2469)

<223>

<400> 32  
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 Met Asp Gln Ile Glu Ile Ile Lys Thr Ile Asn Ser Met Ile Glu Tyr  
 1 5 10 15

ata aaa aat acc aaa gat aag tta tct ata gat aat ttt ata ttc gaa 96  
 Ile Lys Asn Thr Lys Asp Lys Leu Ser Ile Asp Asn Phe Ile Phe Glu

20	25	30	
cat aaa gat tta tat gat aat gta gtt att tat tca aaa tat tta tca			144
His Lys Asp Leu Tyr Asp Asn Val Val Ile Tyr Ser Lys Tyr Leu Ser			
35	40	45	
gat aaa gat ttt aaa ttt tta tac gtt att gta gaa aaa tat cca gac			192
Asp Lys Asp Phe Lys Phe Leu Tyr Val Ile Val Glu Lys Tyr Pro Asp			
50	55	60	
gca aat cca aat ata ata tat aat ata ttt aaa aca tca cag ata tct			240
Ala Asn Pro Asn Ile Ile Tyr Asn Ile Phe Lys Thr Ser Gln Ile Ser			
65	70	75	80
ata acg caa gat att aat ata aat aaa ata ata cag aat aaa gat aat			288
Ile Thr Gln Asp Ile Asn Ile Asn Lys Ile Ile Gln Asn Lys Asp Asn			
85	90	95	
aca aaa ata aac caa gat ata cac aca tat aat tat ttg tta tta tta			336
Thr Lys Ile Asn Gln Asp Ile His Thr Tyr Asn Tyr Leu Leu Leu Leu			
100	105	110	
aat aaa tta tat ata ttt caa cca ata cca aaa ttt ata aat ata tta			384
Asn Lys Leu Tyr Ile Phe Gln Pro Ile Pro Lys Phe Ile Asn Ile Leu			
115	120	125	
tgg gat ata aaa tca aaa aat gta gat aat cta gac aaa ata aat aat			432
Trp Asp Ile Lys Ser Lys Asn Val Asp Asn Leu Asp Lys Ile Asn Asn			
130	135	140	
ata aat aca aat tcg tta aat ata att aca aat ata gaa atg tca aaa			480
Ile Asn Thr Asn Ser Leu Asn Ile Ile Thr Asn Ile Glu Met Ser Lys			
145	150	155	160
gtt aat att att tat ata tca ttt aca tat att tca tct tat ata gaa			528
Val Asn Ile Ile Tyr Ile Ser Phe Thr Tyr Ile Ser Ser Tyr Ile Glu			
165	170	175	
tca cat aaa agt gaa ctt acg tta aat aaa aaa ttt tct att tat gat			576
Ser His Lys Ser Glu Leu Thr Leu Asn Lys Lys Phe Ser Ile Tyr Asp			
180	185	190	
aat tta aga aga ata att ggc gtt cct ata tct aat aat aac tat aaa			624
Asn Leu Arg Arg Ile Ile Gly Val Pro Ile Ser Asn Asn Asn Tyr Lys			
195	200	205	
tta aat tat tat att aaa gct aaa ata gat tca gaa aca tta ata tat			672
Leu Asn Tyr Tyr Ile Lys Ala Lys Ile Asp Ser Glu Thr Leu Ile Tyr			
210	215	220	
aat ata ttt aat tct gta gct ttt aaa aaa gta ata ata tat gga ttt			720
Asn Ile Phe Asn Ser Val Ala Phe Lys Lys Val Ile Ile Tyr Gly Phe			
225	230	235	240
gga gtt tat caa ata aaa gat gta aaa aat ata ata aaa gat acg att			768
Gly Val Tyr Gln Ile Lys Asp Val Lys Asn Ile Ile Lys Asp Thr Ile			
245	250	255	

aat gat gtt tcg tca tac ata gtt aat aat aat aaa gaa aaa ttg tat	816
Asn Asp Val Ser Ser Tyr Ile Val Asn Asn Asn Lys Glu Lys Leu Tyr	
260 265 270	
caa cgt aca tac tgt tgt tgt tat ttt tta aac tgt tat tat gaa aaa	864
Gln Arg Thr Tyr Cys Cys Cys Tyr Phe Leu Asn Cys Tyr Tyr Glu Lys	
275 280 285	
att ttt aaa aat tta tcc aca caa aca tat gat aaa ata tta tat tca	912
Ile Phe Lys Asn Leu Ser Thr Gln Thr Tyr Asp Lys Ile Leu Tyr Ser	
290 295 300	
aat gta gtt aat att aat gat gtt att cat aaa aaa tat gaa tat ttc	960
Asn Val Val Asn Ile Asn Asp Val Ile His Lys Lys Tyr Glu Tyr Phe	
305 310 315 320	
gaa tgt caa cat gta caa gaa tat aaa aat gtt ttt aaa aat gta gaa	1008
Glu Cys Gln His Val Gln Glu Tyr Lys Asn Val Phe Lys Asn Val Glu	
325 330 335	
aat ttt tat att aat act aat aaa ttt cta gaa aat tat att aat att	1056
Asn Phe Tyr Ile Asn Thr Asn Lys Phe Leu Glu Asn Tyr Ile Asn Ile	
340 345 350	
gtt aat aaa gta gct ata tgt aaa att tgt gga gaa tcg tta gat atg	1104
Val Asn Lys Val Ala Ile Cys Lys Ile Cys Gly Glu Ser Leu Asp Met	
355 360 365	
ttt aat ttt gaa gaa gca aat tat att caa tct aaa ggc gaa att ata	1152
Phe Asn Phe Glu Glu Ala Asn Tyr Ile Gln Ser Lys Gly Glu Ile Ile	
370 375 380	
ata aca aca aat aaa gaa aat att ttc caa tat gaa act tat tca aga	1200
Ile Thr Thr Asn Lys Glu Asn Ile Phe Gln Tyr Glu Thr Tyr Ser Arg	
385 390 395 400	
tta gtt aat gct gaa tta ttt tta aca gat att ata gga att tat gat	1248
Leu Val Asn Ala Glu Leu Phe Leu Thr Asp Ile Ile Gly Ile Tyr Asp	
405 410 415	
gat att ttt aac aca aac aga atg gac gat ttt aat aat ata tct aga	1296
Asp Ile Phe Asn Thr Asn Arg Met Asp Asp Phe Asn Asn Ile Ser Arg	
420 425 430	
ata att att gat ttt ttt att gat att aac aca aat aga tta gaa tat	1344
Ile Ile Ile Asp Phe Phe Ile Asp Ile Asn Thr Asn Arg Leu Glu Tyr	
435 440 445	
caa gat aaa tat aaa aaa caa atc tct aac tcc aaa tta ttt ttt ata	1392
Gln Asp Lys Tyr Lys Lys Gln Ile Ser Asn Ser Lys Leu Phe Phe Ile	
450 455 460	
aga ttg tca aat aat tta ttt ata gca gtt tat aat gaa aaa gaa caa	1440
Arg Leu Ser Asn Asn Leu Phe Ile Ala Val Tyr Asn Glu Lys Glu Gln	
465 470 475 480	

tat gcc gaa gaa aga caa cta aac atg ttt ata ata ttc gga ata tct	1488
Tyr Ala Glu Glu Arg Gln Leu Asn Met Phe Ile Ile Phe Gly Ile Ser	
485 490 495	
tta tta tta tta agt aat ttt aat gaa tta ata ggt ata ata aaa aat	1536
Leu Leu Leu Leu Ser Asn Phe Asn Glu Leu Ile Gly Ile Ile Lys Asn	
500 505 510	
aat aaa aaa tta aaa act ata ttt gat aat caa aat gat att aaa ata	1584
Asn Lys Lys Leu Lys Thr Ile Phe Asp Asn Gln Asn Asp Ile Lys Ile	
515 520 525	
aat tta gat aat ttt ata aaa gat act gta ttc ata tat ata agt agg	1632
Asn Leu Asp Asn Phe Ile Lys Asp Thr Val Phe Ile Tyr Ile Ser Arg	
530 535 540	
aat aga tta ata gat aaa aaa agt aga gaa ttg att aat tat gat act	1680
Asn Arg Leu Ile Asp Lys Lys Ser Arg Glu Leu Ile Asn Tyr Asp Thr	
545 550 555 560	
ata att gat gtt tat tta aat ata tta act ccc gaa tta aaa tcg tgt	1728
Ile Ile Asp Val Tyr Leu Asn Ile Leu Thr Pro Glu Leu Lys Ser Cys	
565 570 575	
tat aat ata ata tta aat aga tta tat aaa aat ata gat att tta aaa	1776
Tyr Asn Ile Ile Leu Asn Arg Leu Tyr Lys Asn Ile Asp Ile Leu Lys	
580 585 590	
tat gat tat ata gaa tta cca gat att cca tta cta ccc gta aca tta	1824
Tyr Asp Tyr Ile Glu Leu Pro Asp Ile Pro Leu Leu Pro Val Thr Leu	
595 600 605	
gga tat aaa cac aaa aat att gat act ggt cct aca ata tct ttt tta	1872
Gly Tyr Lys His Lys Asn Ile Asp Thr Gly Pro Thr Ile Ser Phe Leu	
610 615 620	
cca ctc gaa gat gta att aat tat aat aat gta aat att tat gaa agt	1920
Pro Leu Glu Asp Val Ile Asn Tyr Asn Asn Val Asn Ile Tyr Glu Ser	
625 630 635 640	
aat att aga tat att aca tac gat acg tta aaa att aaa aat tta tct	1968
Asn Ile Arg Tyr Ile Thr Tyr Asp Thr Leu Lys Ile Lys Asn Leu Ser	
645 650 655	
gat ttt gat att aaa gat ata aat gtt gaa tta aaa act ata att gaa	2016
Asp Phe Asp Ile Lys Asp Ile Asn Val Glu Leu Lys Thr Ile Ile Glu	
660 665 670	
aga ttt aat tct gaa tat tac tat aga aat att agt ata tta aac ttt	2064
Arg Phe Asn Ser Glu Tyr Tyr Tyr Arg Asn Ile Ser Ile Leu Asn Phe	
675 680 685	
gaa cag atg gat aat tat aat ttt tat ata gat ata gga caa aaa tat	2112
Glu Gln Met Asp Asn Tyr Asn Phe Tyr Ile Asp Ile Gly Gln Lys Tyr	
690 695 700	
ttt ttt tat ata aat gat gta tta tcg aat agt aat att gta ata aaa	2160

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Phe Phe Tyr Ile Asn Asp Val Leu Ser Asn Ser Asn Ile Val Ile Lys
705                710                715                720

agt aat att tat tct aaa ata atg aat ttt ggt gat tct ttg cca ttt      2208
Ser Asn Ile Tyr Ser Lys Ile Met Asn Phe Gly Asp Ser Leu Pro Phe
              725                730                735

tta aat aaa ata tat aaa ttt cat tat aca tta tta ttt gat aat ctg      2256
Leu Asn Lys Ile Tyr Lys Phe His Tyr Thr Leu Leu Phe Asp Asn Leu
              740                745                750

aat tta tta ata aat ttt tta tat ccg aat gtt aaa att ata ttt aat      2304
Asn Leu Leu Ile Asn Phe Leu Tyr Pro Asn Val Lys Ile Ile Phe Asn
              755                760                765

tat gat caa gat tat ata act aga gat tat ttt cat tat att gtt tat      2352
Tyr Asp Gln Asp Tyr Ile Thr Arg Asp Tyr Phe His Tyr Ile Val Tyr
              770                775                780

aat ata tta att tca tta att aat act aat ata tta tca tgg ata gat      2400
Asn Ile Leu Ile Ser Leu Ile Asn Thr Asn Ile Leu Ser Trp Ile Asp
785                790                795                800

gta aac aaa gat ata ata tct aaa tta tat gat aat act tta aga ttt      2448
Val Asn Lys Asp Ile Ile Ser Lys Leu Tyr Asp Asn Thr Leu Arg Phe
              805                810                815

tat gtt aaa aat ata tat taa      2469
Tyr Val Lys Asn Ile Tyr
              820

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<210> 33

<211> 1410

<212> DNA

<213> Amsacta moorei entomopoxvirus

<220>

<221> exon

<222> (1)..(1410)

<223>

<400> 33

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atg gtt aaa tat att aaa tta aat aaa aaa ata ttt aat tat ata aaa      48
Met Val Lys Tyr Ile Lys Leu Asn Lys Lys Ile Phe Asn Tyr Ile Lys
1                5                10                15

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tca aga tta aaa tca caa gaa ata tta ata tat gat aaa aat tct aat	96
Ser Arg Leu Lys Ser Gln Glu Ile Leu Ile Tyr Asp Lys Asn Ser Asn	
20 25 30	
cat gct ata att aca aat gat atg ata gaa aat att gat tta gat ata	144
His Ala Ile Ile Thr Asn Asp Met Ile Glu Asn Ile Asp Leu Asp Ile	
35 40 45	
ata tgt ccg ttg att ttg tat aac gaa aat gat aaa att att gac aaa	192
Ile Cys Pro Leu Ile Leu Tyr Asn Glu Asn Asp Lys Ile Ile Asp Lys	
50 55 60	
att aat aat atg gat aaa ttt att gag tgt aaa tat caa tta agg gaa	240
Ile Asn Asn Met Asp Lys Phe Ile Glu Cys Lys Tyr Gln Leu Arg Glu	
65 70 75 80	
gat caa tta gag tta att aat aat ata atg aat att aat aat aat tat	288
Asp Gln Leu Glu Leu Ile Asn Asn Ile Met Asn Ile Asn Asn Asn Tyr	
85 90 95	
tct tgt aat tca ccc ata tat tta tca tta gta tgt cct tgt gga tat	336
Ser Cys Asn Ser Pro Ile Tyr Leu Ser Leu Val Cys Pro Cys Gly Tyr	
100 105 110	
ggg aaa act ata ttg ggt ata gat ata ata tct aga tta aaa tac aaa	384
Gly Lys Thr Ile Leu Gly Ile Asp Ile Ile Ser Arg Leu Lys Tyr Lys	
115 120 125	
tgt gct ata att gta cct aga att ttt att ata tat caa tgg tta gat	432
Cys Ala Ile Ile Val Pro Arg Ile Phe Ile Ile Tyr Gln Trp Leu Asp	
130 135 140	
aaa ata aaa caa aaa aat aat ata ttt gca tct acg tgt ggt aga aaa	480
Lys Ile Lys Gln Lys Asn Asn Ile Phe Ala Ser Thr Cys Gly Arg Lys	
145 150 155 160	
aaa gcg att gaa caa ata aaa aat ggt tta gag tgt gat gtg ttt ata	528
Lys Ala Ile Glu Gln Ile Lys Asn Gly Leu Glu Cys Asp Val Phe Ile	
165 170 175	
tgt cct gat aaa cat tta gaa aat gat att att aga aat tat ata tat	576
Cys Pro Asp Lys His Leu Glu Asn Asp Ile Ile Arg Asn Tyr Ile Tyr	
180 185 190	
aat acg tgt agt tta gta att gtt gat gaa gct cat cga tat aat gct	624
Asn Thr Cys Ser Leu Val Ile Val Asp Glu Ala His Arg Tyr Asn Ala	
195 200 205	
aat aaa aat ata gta atg act aga ttt tta tat aat aaa ata ttt aaa	672
Asn Lys Asn Ile Val Met Thr Arg Phe Leu Tyr Asn Lys Ile Phe Lys	
210 215 220	
ttt tgt ttg ttt tta act gct acg cca tct aat aat atg aat act ttt	720
Phe Cys Leu Phe Leu Thr Ala Thr Pro Ser Asn Asn Met Asn Thr Phe	
225 230 235 240	
ata aat gaa ttt att gat att aat aat caa tca cag att aaa ata tta	768



Ile Asn Glu Phe Ile Asp Ile Asn Asn Gln Ser Gln Ile Lys Ile Leu	
245 250 255	
aat gat att aaa aaa aaa tta att ata ttt aat ttg aaa gat aaa ata	816
Asn Asp Ile Lys Lys Lys Leu Ile Ile Phe Asn Leu Lys Asp Lys Ile	
260 265 270	
ttt act cca att aat aat aat tgt aaa tat tat gtt aat aaa ata aca	864
Phe Thr Pro Ile Asn Asn Asn Cys Lys Tyr Tyr Val Asn Lys Ile Thr	
275 280 285	
aat aat aaa ttc aat aat ata tat ata aaa aat ttt aat tac aaa tat	912
Asn Asn Lys Phe Asn Asn Ile Tyr Ile Lys Asn Phe Asn Tyr Lys Tyr	
290 295 300	
tgt att tct ctt gat gat aaa aga aat gaa att att ata gat tta ata	960
Cys Ile Ser Leu Asp Asp Lys Arg Asn Glu Ile Ile Ile Asp Leu Ile	
305 310 315 320	
tta aaa aca act acg gat aat aca aaa tgt tta att ttg aca gat tat	1008
Leu Lys Thr Thr Thr Asp Asn Thr Lys Cys Leu Ile Leu Thr Asp Tyr	
325 330 335	
aga tta cac atg atg aat ata tat aat tta tta aaa aaa aca cac tta	1056
Arg Leu His Met Met Asn Ile Tyr Asn Leu Leu Lys Lys Thr His Leu	
340 345 350	
caa aat ata att tat ata tat gat gta aaa aat aaa aaa tgt aat gat	1104
Gln Asn Ile Ile Tyr Ile Tyr Asp Val Lys Asn Lys Lys Cys Asn Asp	
355 360 365	
ttg tta aca gaa att aaa aat aag aat gaa aaa ttt att att ata tca	1152
Leu Leu Thr Glu Ile Lys Asn Lys Asn Glu Lys Phe Ile Ile Ile Ser	
370 375 380	
act ata tct gct tgt tct gaa tca tta gat att aat aat tta aat act	1200
Thr Ile Ser Ala Cys Ser Glu Ser Leu Asp Ile Asn Asn Leu Asn Thr	
385 390 395 400	
ttt cat gtt tta tta cct att act aat tct aaa aca ata aaa caa tgc	1248
Phe His Val Leu Leu Pro Ile Thr Asn Ser Lys Thr Ile Lys Gln Cys	
405 410 415	
ata ggt aga att atg aga aat atg aac gaa gat aaa tat act tat ata	1296
Ile Gly Arg Ile Met Arg Asn Met Asn Glu Asp Lys Tyr Thr Tyr Ile	
420 425 430	
tat aat ttt tct aac atc aat aac atg att aat atg tat att aat gat	1344
Tyr Asn Phe Ser Asn Ile Asn Asn Met Ile Asn Met Tyr Ile Asn Asp	
435 440 445	
aaa act gat tta ata aga aaa gta ttg tct gat tgg gaa tgt gta gaa	1392
Lys Thr Asp Leu Ile Arg Lys Val Leu Ser Asp Trp Glu Cys Val Glu	
450 455 460	
ata aaa tgt tca tat taa	1410
Ile Lys Cys Ser Tyr	

465

&lt;210&gt; 34

&lt;211&gt; 768

&lt;212&gt; DNA

&lt;213&gt; Amsacta moorei entomopoxvirus

&lt;220&gt;

&lt;221&gt; exon

&lt;222&gt; (1)..(768)

&lt;223&gt;

&lt;400&gt; 34

atg	tat	tgt	aac	cca	ata	gca	ttt	ata	tct	gat	ttt	gat	aat	tca	tac	48
Met	Tyr	Cys	Asn	Pro	Ile	Ala	Phe	Ile	Ser	Asp	Phe	Asp	Asn	Ser	Tyr	
1			5					10					15			

gct	ggt	aga	gtt	aga	tac	ata	gat	aat	ttt	ata	gct	gga	gct	aca	aat	96
Ala	Gly	Arg	Val	Arg	Tyr	Ile	Asp	Asn	Phe	Ile	Ala	Gly	Ala	Thr	Asn	
			20					25					30			

att	cca	gat	aat	aaa	act	att	ttt	aaa	ata	att	gga	gga	aaa	ggt	gtt	144
Ile	Pro	Asp	Asn	Lys	Thr	Ile	Phe	Lys	Ile	Ile	Gly	Gly	Lys	Gly	Val	
			35					40					45			

ttt	tta	aaa	act	aat	agt	caa	tat	aac	act	ata	cca	tat	aca	tca	cct	192
Phe	Leu	Lys	Thr	Asn	Ser	Gln	Tyr	Asn	Thr	Ile	Pro	Tyr	Thr	Ser	Pro	
	50						55				60					

act	aaa	aaa	aaa	aat	aat	tac	tta	gtc	tat	aat	ata	tat	gat	ttg	cga	240
Thr	Lys	Lys	Lys	Asn	Asn	Tyr	Leu	Val	Tyr	Asn	Ile	Tyr	Asp	Leu	Arg	
65					70					75				80		

gat	tat	att	agt	gaa	aat	tca	aaa	ttc	tcg	ata	aat	gat	ttt	atg	aat	288
Asp	Tyr	Ile	Ser	Glu	Asn	Ser	Lys	Phe	Ser	Ile	Asn	Asp	Phe	Met	Asn	
				85					90					95		

aat	att	aat	aat	tcg	tca	caa	aat	aat	aga	att	atg	gtt	ctg	agt	ggt	336
Asn	Ile	Asn	Asn	Ser	Ser	Gln	Asn	Asn	Arg	Ile	Met	Val	Leu	Ser	Gly	
			100					105					110			

gat	aca	aaa	tat	aaa	ata	aga	aat	cct	aat	aga	tta	ata	ttt	tct	gat	384
Asp	Thr	Lys	Tyr	Lys	Ile	Arg	Asn	Pro	Asn	Arg	Leu	Ile	Phe	Ser	Asp	
		115					120					125				

aca	tct	tat	cct	att	tta	gtt	act	tat	aat	tta	aat	gat	aaa	att	aat	432
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Thr	Ser	Tyr	Pro	Ile	Leu	Val	Thr	Tyr	Asn	Leu	Asn	Asp	Lys	Ile	Asn		
130						135					140						
ata	tct	atc	gaa	aac	cca	aat	gaa	aaa	gta	gaa	aaa	tat	gaa	ata	ccc	480	
Ile	Ser	Ile	Glu	Asn	Pro	Asn	Glu	Lys	Val	Glu	Lys	Tyr	Glu	Ile	Pro		
145					150					155					160		
gaa	gat	gtt	tgc	tat	gtc	tat	aaa	caa	aaa	gat	aca	tat	gta	atg	tcg	528	
Glu	Asp	Val	Cys	Tyr	Val	Tyr	Lys	Gln	Lys	Asp	Thr	Tyr	Val	Met	Ser		
				165					170					175			
gtt	aat	gtt	aaa	cgt	ttg	acg	cca	gta	gat	ata	tat	tat	att	act	acc	576	
Val	Asn	Val	Lys	Arg	Leu	Thr	Pro	Val	Asp	Ile	Tyr	Tyr	Ile	Thr	Thr		
			180				185						190				
gaa	gtt	gat	caa	aat	aat	tca	aat	aat	ata	aaa	tct	ata	aaa	ata	gaa	624	
Glu	Val	Asp	Gln	Asn	Asn	Ser	Asn	Asn	Ile	Lys	Ser	Ile	Lys	Ile	Glu		
		195					200					205					
gat	aca	tca	gaa	cct	tta	gaa	ata	cac	cca	tct	tat	aga	aaa	ata	tta	672	
Asp	Thr	Ser	Glu	Pro	Leu	Glu	Ile	His	Pro	Ser	Tyr	Arg	Lys	Ile	Leu		
	210					215					220						
gta	aca	aaa	tta	gtg	gat	ttt	att	aat	caa	aat	ata	aaa	cca	act	aat	720	
Val	Thr	Lys	Leu	Val	Asp	Phe	Ile	Asn	Gln	Asn	Ile	Lys	Pro	Thr	Asn		
225					230					235					240		
ttt	aat	ttt	tca	gaa	tat	ttt	gat	aag	tat	ata	aat	act	act	aaa	taa	768	
Phe	Asn	Phe	Ser	Glu	Tyr	Phe	Asp	Lys	Tyr	Ile	Asn	Thr	Thr	Lys			
				245					250					255			

&lt;210&gt; 35

&lt;211&gt; 3591

&lt;212&gt; DNA

&lt;213&gt; Amsacta moorei entomopoxvirus

&lt;220&gt;

&lt;221&gt; exon

&lt;222&gt; (1)..(3591)

&lt;223&gt;

&lt;400&gt; 35

atg	aat	aat	aat	ccg	att	gaa	gaa	gat	att	gca	aat	tta	ttt	ttg	caa	48	
Met	Asn	Asn	Asn	Pro	Ile	Glu	Glu	Asp	Ile	Ala	Asn	Leu	Phe	Leu	Gln		
1				5					10					15			

tgc gat cct aga ttg gat ata aaa tct aaa gtt ttg att aat gta gaa	96
Cys Asp Pro Arg Leu Asp Ile Lys Ser Lys Val Leu Ile Asn Val Glu	
20 25 30	
tta cca ttt aaa aat tta aat tat gat ttg cct acg tta ttt aat aga	144
Leu Pro Phe Lys Asn Leu Asn Tyr Asp Leu Pro Thr Leu Phe Asn Arg	
35 40 45	
gaa gaa gtt ata tat aca aag ata agt aaa tca gga cat gaa gat gtc	192
Glu Glu Val Ile Tyr Thr Lys Ile Ser Lys Ser Gly His Glu Asp Val	
50 55 60	
ata atg aaa ata aca tac gaa ggt aaa gaa gat aat aaa aaa agt tat	240
Ile Met Lys Ile Thr Tyr Glu Gly Lys Glu Asp Asn Lys Lys Ser Tyr	
65 70 75 80	
tta tat tcc agt tta gat aat aaa gga ttt tat aca tat atc tct att	288
Leu Tyr Ser Ser Leu Asp Asn Lys Gly Phe Tyr Thr Tyr Ile Ser Ile	
85 90 95	
tct att tct ata tat aga aaa ata aca tca tta aat aat aaa ata gaa	336
Ser Ile Ser Ile Tyr Arg Lys Ile Thr Ser Leu Asn Asn Lys Ile Glu	
100 105 110	
tat aaa ata ata tct aat aaa aca tat tcg cat aca gaa ata aga ata	384
Tyr Lys Ile Ile Ser Asn Lys Thr Tyr Ser His Thr Glu Ile Arg Ile	
115 120 125	
cct cag tat ata gct cac ggt gga aat aca tca gaa aat gat aat tct	432
Pro Gln Tyr Ile Ala His Gly Gly Asn Thr Ser Glu Asn Asp Asn Ser	
130 135 140	
ata aca caa tca aat aat cct ggt gga ttt ttt aat gtt tca aaa agt	480
Ile Thr Gln Ser Asn Asn Pro Gly Gly Phe Phe Asn Val Ser Lys Ser	
145 150 155 160	
tta aaa aaa atg gta act act aga ata gaa caa aca tat att tat cca	528
Leu Lys Lys Met Val Thr Thr Arg Ile Glu Gln Thr Tyr Ile Tyr Pro	
165 170 175	
aaa cgt aaa aaa act caa aaa gca tat act tat cat ctg gca ttc att	576
Lys Arg Lys Lys Thr Gln Lys Ala Tyr Thr Tyr His Leu Ala Phe Ile	
180 185 190	
agt aaa aaa cca tca ttt atg atg ata aat gaa aaa tta aac ccg cca	624
Ser Lys Lys Pro Ser Phe Met Met Ile Asn Glu Lys Leu Asn Pro Pro	
195 200 205	
cag ttt tta act tta gat ata gat ttt aat cca gat aaa ata aaa tgt	672
Gln Phe Leu Thr Leu Asp Ile Asp Phe Asn Pro Asp Lys Ile Lys Cys	
210 215 220	
gta ata gat tct aaa aaa aca ttc tta caa att gat atc ata gca tta	720
Val Ile Asp Ser Lys Lys Thr Phe Leu Gln Ile Asp Ile Ile Ala Leu	
225 230 235 240	
ata ata gca tta tct aat gat aac att gat gtt gtt tat aaa aaa ata	768

Ile	Ile	Ala	Leu	Ser	Asn	Asp	Asn	Ile	Asp	Val	Val	Tyr	Lys	Lys	Ile		
				245					250					255			
agt	tct	ggg	ttt	agt	gat	gat	ata	tct	gat	tca	atc	aaa	ata	tta	ata	816	
Ser	Ser	Gly	Phe	Ser	Asp	Asp	Ile	Ser	Asp	Ser	Ile	Lys	Ile	Leu	Ile		
			260					265					270				
gaa	aat	act	aaa	aat	att	tta	tct	gaa	tat	aat	aat	gat	gcc	aga	caa	864	
Glu	Asn	Thr	Lys	Asn	Ile	Leu	Ser	Glu	Tyr	Asn	Asn	Asp	Ala	Arg	Gln		
			275					280				285					
tat	gtc	gac	aaa	ata	atc	gaa	att	aat	tat	att	aaa	aaa	tat	cca	aaa	912	
Tyr	Val	Asp	Lys	Ile	Ile	Glu	Ile	Asn	Tyr	Ile	Lys	Lys	Tyr	Pro	Lys		
	290						295				300						
aat	gaa	ata	act	tta	caa	gat	tat	ttt	aat	aat	att	ttc	aat	gat	ttt	960	
Asn	Glu	Ile	Thr	Leu	Gln	Asp	Tyr	Phe	Asn	Asn	Ile	Phe	Asn	Asp	Phe		
305					310					315					320		
ctt	cct	cat	ata	ggc	cga	gga	aaa	tat	aat	gaa	aaa	tgt	atg	tat	atg	1008	
Leu	Pro	His	Ile	Gly	Arg	Gly	Lys	Tyr	Asn	Glu	Lys	Cys	Met	Tyr	Met		
				325					330					335			
att	agt	att	tta	aga	caa	tct	ttt	gtt	tct	ata	ttt	caa	tca	gat	gtt	1056	
Ile	Ser	Ile	Leu	Arg	Gln	Ser	Phe	Val	Ser	Ile	Phe	Gln	Ser	Asp	Val		
			340					345					350				
tat	cca	gat	aaa	gat	aat	tta	gct	act	aga	aga	att	tca	act	gct	gct	1104	
Tyr	Pro	Asp	Lys	Asp	Asn	Leu	Ala	Thr	Arg	Arg	Ile	Ser	Thr	Ala	Ala		
		355					360					365					
gat	att	ttt	gag	aat	ata	ata	agg	act	tct	att	gat	aat	tct	ttc	gaa	1152	
Asp	Ile	Phe	Glu	Asn	Ile	Ile	Arg	Thr	Ser	Ile	Asp	Asn	Ser	Phe	Glu		
	370					375					380						
tta	gca	aga	gat	aaa	tat	aaa	aca	tat	att	agt	gga	tct	ggg	aag	aac	1200	
Leu	Ala	Arg	Asp	Lys	Tyr	Lys	Thr	Tyr	Ile	Ser	Gly	Ser	Gly	Lys	Asn		
385					390					395					400		
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Asn	Asn	Ile	Asn	Asn	Ile	Leu	Ser	Gln	Val	Lys	Leu	Leu	Pro	Gln	Ile		
				405					410					415			
aca	caa	gcg	ttt	aat	aat	ttt	ttc	aat	atg	caa	gat	act	aaa	aat	agt	1296	
Thr	Gln	Ala	Phe	Asn	Asn	Phe	Phe	Asn	Met	Gln	Asp	Thr	Lys	Asn	Ser		
			420					425					430				
gat	gtt	gta	aaa	ata	gga	acc	cac	tca	aat	tgg	gct	gaa	tct	att	tat	1344	
Asp	Val	Val	Lys	Ile	Gly	Thr	His	Ser	Asn	Trp	Ala	Glu	Ser	Ile	Tyr		
		435					440					445					
att	tct	aat	gct	gta	gaa	aga	ggg	gtt	agt	ata	gaa	tta	aca	aaa	tca	1392	
Ile	Ser	Asn	Ala	Val	Glu	Arg	Gly	Val	Ser	Ile	Glu	Leu	Thr	Lys	Ser		
	450					455					460						
cta	act	caa	aga	aaa	tta	cac	gca	tca	tca	att	aat	gta	tta	gat	atg	1440	
Leu	Thr	Gln	Arg	Lys	Leu	His	Ala	Ser	Ser	Ile	Asn	Val	Leu	Asp	Met		

465	470	475	480	
atg gat aca cct gat cat ggt aca aaa act ggt ctt gta aaa aga tta				1488
Met Asp Thr Pro Asp His Gly Thr Lys Thr Gly Leu Val Lys Arg Leu	485	490	495	
tgt ata agt aca tta ata tca cac tat cct ata cat att aga aaa caa				1536
Cys Ile Ser Thr Leu Ile Ser His Tyr Pro Ile His Ile Arg Lys Gln	500	505	510	
tta ttt gaa gaa gtt aga gaa ttt ata gaa aac aag gtt aaa cat aca				1584
Leu Phe Glu Glu Val Arg Glu Phe Ile Glu Asn Lys Val Lys His Thr	515	520	525	
tta aaa gaa gat att att tcc ggt gta ttt ata tca att ata gat gaa				1632
Leu Lys Glu Asp Ile Ile Ser Gly Val Phe Ile Ser Ile Ile Asp Glu	530	535	540	
tct gaa cac gta ata gct cgt ata aaa aat tca gaa act gaa tct ttt				1680
Ser Glu His Val Ile Ala Arg Ile Lys Asn Ser Glu Thr Glu Ser Phe	545	550	555	560
ata aaa gat tta aaa tat gca aaa ata tca gga tta ttt gtt aaa aat				1728
Ile Lys Asp Leu Lys Tyr Ala Lys Ile Ser Gly Leu Phe Val Lys Asn	565	570	575	
gat ata ggt ata gaa ata tta aaa ttt cat gaa tta gat aat aac aaa				1776
Asp Ile Gly Ile Glu Ile Leu Lys Phe His Glu Leu Asp Asn Asn Lys	580	585	590	
caa ata tat gta cca aca gat aga tat ttt caa ata aga ata aat gtt				1824
Gln Ile Tyr Val Pro Thr Asp Arg Tyr Phe Gln Ile Arg Ile Asn Val	595	600	605	
ggt aat aaa aga gca aca caa cca gta ttt aga gta gaa aat ggc gaa				1872
Gly Asn Lys Arg Ala Thr Gln Pro Val Phe Arg Val Glu Asn Gly Glu	610	615	620	
tta gca ttt aat aaa tat cct aat tta cat gct gaa tta aaa gag agt				1920
Leu Ala Phe Asn Lys Tyr Pro Asn Leu His Ala Glu Leu Lys Glu Ser	625	630	635	640
aat tct tac act gat ttt gta act aaa tat tat gat att ata gaa gtt				1968
Asn Ser Tyr Thr Asp Phe Val Thr Lys Tyr Tyr Asp Ile Ile Glu Val	645	650	655	
att gac gta gga caa atg ata tat tca aat atg tgt aac aca gtt aca				2016
Ile Asp Val Gly Gln Met Ile Tyr Ser Asn Met Cys Asn Thr Val Thr	660	665	670	
gaa ttt aat agt tac agt tta gaa caa aga aaa aaa tat gat tat gtt				2064
Glu Phe Asn Ser Tyr Ser Leu Glu Gln Arg Lys Lys Tyr Asp Tyr Val	675	680	685	
aga tta cca aat tat tta tat ttt agt tat tta aca tcg act ggt tgt				2112
Arg Leu Pro Asn Tyr Leu Tyr Phe Ser Tyr Leu Thr Ser Thr Gly Cys	690	695	700	

atg tat gat att ggt aaa atg acg ggt gtt aga ggt aca ttt gga aca	2160
Met Tyr Asp Ile Gly Lys Met Thr Gly Val Arg Gly Thr Phe Gly Thr	
705 710 715 720	
gcc caa agt aaa cat att ata aca gga cct cca gat aat gta atg aat	2208
Ala Gln Ser Lys His Ile Ile Thr Gly Pro Pro Asp Asn Val Met Asn	
725 730 735	
aaa tat gat aca tgt aac tat tta gca tat cct ata gaa aga cca tca	2256
Lys Tyr Asp Thr Cys Asn Tyr Leu Ala Tyr Pro Ile Glu Arg Pro Ser	
740 745 750	
ata act aat att cct atg gaa ata tct ggt ata gca aga aat agt ata	2304
Ile Thr Asn Ile Pro Met Glu Ile Ser Gly Ile Ala Arg Asn Ser Ile	
755 760 765	
ggg aca cat gtt tta gtg gga ttc ttt agt ttt aat tac aac gta gaa	2352
Gly Thr His Val Leu Val Gly Phe Phe Ser Phe Asn Tyr Asn Val Glu	
770 775 780	
gat ggc gtt att gta aat aaa gaa tcg ata aat aga gga tta tta tct	2400
Asp Gly Val Ile Val Asn Lys Glu Ser Ile Asn Arg Gly Leu Leu Ser	
785 790 795 800	
gta ata tca tta atg tct gta aaa aat gaa tta tct gat aca caa ata	2448
Val Ile Ser Leu Met Ser Val Lys Asn Glu Leu Ser Asp Thr Gln Ile	
805 810 815	
aac aat aat aat cca agt gca gaa aat tct aat aat aat tat tct aaa	2496
Asn Asn Asn Asn Pro Ser Ala Glu Asn Ser Asn Asn Asn Tyr Ser Lys	
820 825 830	
ata tca gca aca ggt ttg cca tca ata gga act gtt tta gta caa ggt	2544
Ile Ser Ala Thr Gly Leu Pro Ser Ile Gly Thr Val Leu Val Gln Gly	
835 840 845	
gat gcg tta tac aga tgt tta aaa cca aaa ttt aaa aat gat gat gat	2592
Asp Ala Leu Tyr Arg Cys Leu Lys Pro Lys Phe Lys Asn Asp Asp Asp	
850 855 860	
aat aga tat ata ttt gat caa tct gaa aca cta tct aat act tat cca	2640
Asn Arg Tyr Ile Phe Asp Gln Ser Glu Thr Leu Ser Asn Thr Tyr Pro	
865 870 875 880	
gcc gtg gta gaa aga aca aga aaa caa ggt aca gat tta ata aag att	2688
Ala Val Val Glu Arg Thr Arg Lys Gln Gly Thr Asp Leu Ile Lys Ile	
885 890 895	
gat atg cta ttg tca tca tat aga aga ttg agt gta gga gat aaa ata	2736
Asp Met Leu Leu Ser Ser Tyr Arg Arg Leu Ser Val Gly Asp Lys Ile	
900 905 910	
gca aaa tct gta caa aaa gtt act gtt tca aaa att atg gaa gaa gaa	2784
Ala Lys Ser Val Gln Lys Val Thr Val Ser Lys Ile Met Glu Glu Glu	
915 920 925	

gat atg cct tat aat gaa aat ggc gaa aga cct gat ata ata ttt aat Asp Met Pro Tyr Asn Glu Asn Gly Glu Arg Pro Asp Ile Ile Phe Asn 930 935 940	2832
agt cct agt att ata agt aga aaa act ctt cct ttg tat gac gaa gtt Ser Pro Ser Ile Ile Ser Arg Lys Thr Leu Pro Leu Tyr Asp Glu Val 945 950 955 960	2880
tct tta tgt aat atg ttc tca aaa ata cca tat aat gat aaa tgt gat Ser Leu Cys Asn Met Phe Ser Lys Ile Pro Tyr Asn Asp Lys Cys Asp 965 970 975	2928
gta gaa tat att aat tat cct ata tat act gat aaa agt cct ttg gat Val Glu Tyr Ile Asn Tyr Pro Ile Tyr Thr Asp Lys Ser Pro Leu Asp 980 985 990	2976
aaa tat aat ttt atc aaa aaa gaa tta aaa aaa ata tat aat aat gta Lys Tyr Asn Phe Ile Lys Lys Glu Leu Lys Lys Ile Tyr Asn Asn Val 995 1000 1005	3024
act gac gaa gaa tta gaa aat att ata tat tgt cga caa aca tta Thr Asp Glu Glu Leu Glu Asn Ile Ile Tyr Cys Arg Gln Thr Leu 1010 1015 1020	3069
tat cac cca tat aca aaa aaa cct atg act ata aaa gaa ggt gat Tyr His Pro Tyr Thr Lys Lys Pro Met Thr Ile Lys Glu Gly Asp 1025 1030 1035	3114
aaa gaa act aaa tca ttt atg gga cct atg tta ttc tgt aga tta Lys Glu Thr Lys Ser Phe Met Gly Pro Met Leu Phe Cys Arg Leu 1040 1045 1050	3159
tca caa atg tcg gca gat aaa ata tca gta aga aat aga ggc aga Ser Gln Met Ser Ala Asp Lys Ile Ser Val Arg Asn Arg Gly Arg 1055 1060 1065	3204
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ggt att aaa atc gga gaa atg gaa agt gat gtt ttt gct aca aat Gly Ile Lys Ile Gly Glu Met Glu Ser Asp Val Phe Ala Thr Asn 1085 1090 1095	3294
gga tct gta tat gca ata cat gaa tta caa tca gat cct gat gaa Gly Ser Val Tyr Ala Ile His Glu Leu Gln Ser Asp Pro Asp Glu 1100 1105 1110	3339
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act tat gaa gaa aat ata gaa gta aaa aga tgg aaa tgt cta cag Thr Tyr Glu Glu Asn Ile Glu Val Lys Arg Trp Lys Cys Leu Gln 1130 1135 1140	3429
tgt gaa aat ctt ggt ttg tca cca gaa ata ata aaa atg cgt tta	3474



Cys	Glu	Asn	Leu	Gly	Leu	Ser	Pro	Glu	Ile	Ile	Lys	Met	Arg	Leu	
1145						1150					1155				
act	tat	gct	aca	aaa	ata	ttt	atc	aca	ctt	tta	aat	gct	aga	ggg	3519
Thr	Tyr	Ala	Thr	Lys	Ile	Phe	Ile	Thr	Leu	Leu	Asn	Ala	Arg	Gly	
1160						1165					1170				
ata	tct	cta	atc	cct	gta	aaa	gat	aat	cag	tct	ata	cgt	tat	att	3564
Ile	Ser	Leu	Ile	Pro	Val	Lys	Asp	Asn	Gln	Ser	Ile	Arg	Tyr	Ile	
1175						1180					1185				
tct	gac	gat	aat	act	att	aat	act	taa							3591
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<212> DNA

<213> Amsacta moorei entomopoxvirus

<220>

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1				5				10						15		
aat	cat	agc	aca	gaa	gaa	ata	aaa	aat	ttt	cta	att	gat	aat	aat	att	96
Asn	His	Ser	Thr	Glu	Glu	Ile	Lys	Asn	Phe	Leu	Ile	Asp	Asn	Asn	Ile	
			20				25					30				
aaa	tgt	ata	ata	aca	ata	tg	aat	ttt	aat	aaa	tta	aat	ata	aaa	aaa	144
Lys	Cys	Ile	Ile	Thr	Ile	Trp	Asn	Phe	Asn	Lys	Leu	Asn	Ile	Lys	Lys	
		35				40					45					
tta	aat	att	aat	gtt	aaa	gat	tat	atg	tat	ata	cac	gca	tat	gat	cta	192
Leu	Asn	Ile	Asn	Val	Lys	Asp	Tyr	Met	Tyr	Ile	His	Ala	Tyr	Asp	Leu	
	50				55					60						
aca	aat	gaa	ata	att	att	gat	tat	ttt	gat	att	act	aac	aaa	ttt	ata	240
Thr	Asn	Glu	Ile	Ile	Ile	Asp	Tyr	Phe	Asp	Ile	Thr	Asn	Lys	Phe	Ile	
65					70				75					80		

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att aat aaa ata aaa gaa ggt aag aaa gta tta att cat tgt tat gct      288
Ile Asn Lys Ile Lys Glu Gly Lys Lys Val Leu Ile His Cys Tyr Ala
                        85                      90                      95

ggt ata tca aga tct gca agt ata gtt att aat tat ttt atg aat aaa      336
Gly Ile Ser Arg Ser Ala Ser Ile Val Ile Asn Tyr Phe Met Asn Lys
                        100                      105                      110

tat aat ata aat tat gac gaa gct gaa aaa ata gtt agt aaa aaa cga      384
Tyr Asn Ile Asn Tyr Asp Glu Ala Glu Lys Ile Val Ser Lys Lys Arg
                        115                      120                      125

aat ata aaa cca aat ata ttt ttt ata ctt caa tta aaa ttt tat aat      432
Asn Ile Lys Pro Asn Ile Phe Phe Ile Leu Gln Leu Lys Phe Tyr Asn
                        130                      135                      140

tca tat aaa aat ata aat att att tat tta att ata tta ttt gct att      480
Ser Tyr Lys Asn Ile Asn Ile Ile Tyr Leu Ile Ile Leu Phe Ala Ile
145                      150                      155                      160

aga tat aca cta aaa tga      498
Arg Tyr Thr Leu Lys
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&lt;210&gt; 37

&lt;211&gt; 210

&lt;212&gt; DNA

&lt;213&gt; Amsacta moorei entomopoxvirus

&lt;220&gt;

&lt;221&gt; exon

&lt;222&gt; (1) .. (210)

&lt;223&gt;

&lt;400&gt; 37

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Met Ser Glu Asn Leu Tyr Tyr Val Pro Asp Ile Cys Lys Asn Cys Asn
1                      5                      10                      15

aag tta aat cct aat aat ata ttg gtg ata gac ggt aca tat aga gct      96
Lys Leu Asn Pro Asn Asn Ile Leu Val Ile Asp Gly Thr Tyr Arg Ala
                        20                      25                      30

gcc tat aat gat tat tat tct gtt agt aat aaa ttg cca tct att aaa      144
Ala Tyr Asn Asp Tyr Tyr Ser Val Ser Asn Lys Leu Pro Ser Ile Lys
35                      40                      45

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aca gaa aaa ggt gga tta gca aaa tat cca aaa aaa tta ttt att aga 192  
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aat ggt tat tat aag taa 210  
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<210> 38

<211> 2163

<212> DNA

<213> Amsacta moorei entomopoxvirus

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 1 5 10 15

ccc gaa tta cat aat aaa tat aac tat att tca cat tta tta ttt cct 96  
 Pro Glu Leu His Asn Lys Tyr Asn Tyr Ile Ser His Leu Leu Phe Pro  
 20 25 30

aat aat act aat ata ttt caa tca tat att gat ttt gat tat gta aaa 144  
 Asn Asn Thr Asn Ile Phe Gln Ser Tyr Ile Asp Phe Asp Tyr Val Lys  
 35 40 45

aaa tat aaa tat aat ttt tta ata tta tta tac cct gtt tac aaa cta 192  
 Lys Tyr Lys Tyr Asn Phe Leu Ile Leu Leu Tyr Pro Val Tyr Lys Leu  
 50 55 60

tat tgg aaa aat atg tat att tgt tat aat caa aat agt aat aaa ata 240  
 Tyr Trp Lys Asn Met Tyr Ile Cys Tyr Asn Gln Asn Ser Asn Lys Ile  
 65 70 75 80

tat tta gat aat aaa gaa ata tat aat acc agt att gaa tta att aat 288  
 Tyr Leu Asp Asn Lys Glu Ile Tyr Asn Thr Ser Ile Glu Leu Ile Asn  
 85 90 95

gat ttt tta ata gat gga ata gat ata aat aat aat att ata act att 336  
 Asp Phe Leu Ile Asp Gly Ile Asp Ile Asn Asn Asn Ile Ile Thr Ile

100	105	110	
aga tca aac gga tct aca att act tat tct gca tac gca tat gca aca Arg Ser Asn Gly Ser Thr Ile Thr Tyr Ser Ala Tyr Ala Tyr Ala Thr 115 120 125			384
ata tta tat gat tta cca tat aga tta gga aat tta gat att aat caa Ile Leu Tyr Asp Leu Pro Tyr Arg Leu Gly Asn Leu Asp Ile Asn Gln 130 135 140			432
ata ttt gga att gta gaa agt tct aat ata tta gga ata tta tct aca Ile Phe Gly Ile Val Glu Ser Ser Asn Ile Leu Gly Ile Leu Ser Thr 145 150 155 160			480
aat gaa gaa caa aaa aaa aag ttt cct aaa tat att aat aat ata gaa Asn Glu Glu Gln Lys Lys Lys Phe Pro Lys Tyr Ile Asn Asn Ile Glu 165 170 175			528
tta gaa aaa aat ata tta ttt aaa ttt aag gaa tct aac ctt aga tca Leu Glu Lys Asn Ile Leu Phe Lys Phe Lys Glu Ser Asn Leu Arg Ser 180 185 190			576
ata caa att gat gta caa tta aaa ata ttt gat tta ttt ata aat aga Ile Gln Ile Asp Val Gln Leu Lys Ile Phe Asp Leu Phe Ile Asn Arg 195 200 205			624
tta aat tgt gtt gtt tct ggt gga act ggt ata gga aaa aca tct att Leu Asn Cys Val Val Ser Gly Gly Thr Gly Ile Gly Lys Thr Ser Ile 210 215 220			672
ata cct aaa ata ata tgg tgg tat aat ctt ctt ttt gat gga tat aat Ile Pro Lys Ile Ile Trp Trp Tyr Asn Leu Leu Phe Asp Gly Tyr Asn 225 230 235 240			720
atg ttt aat agt aga att tct aat gta tct ata gat aat ttt ata ttt Met Phe Asn Ser Arg Ile Ser Asn Val Ser Ile Asp Asn Phe Ile Phe 245 250 255			768
gat ata aat ata att gaa aaa aat aca tta tta tca tta cct aga aaa Asp Ile Asn Ile Ile Glu Lys Asn Thr Leu Leu Ser Leu Pro Arg Lys 260 265 270			816
act ata ata aat agt act gct att aat tat ata aaa tca cta ggt tat Thr Ile Ile Asn Ser Thr Ala Ile Asn Tyr Ile Lys Ser Leu Gly Tyr 275 280 285			864
tct gaa ata aca gaa act ccc ata ata ata aaa tat aaa gat ata aaa Ser Glu Ile Thr Glu Thr Pro Ile Ile Ile Lys Tyr Lys Asp Ile Lys 290 295 300			912
tta tat aaa gaa tat tat aat aat aaa att att ttt cca act aat tta Leu Tyr Lys Glu Tyr Tyr Asn Asn Lys Ile Ile Phe Pro Thr Asn Leu 305 310 315 320			960
tta ttg tgt gtt aac aga ttg tca ata aat aat tta aaa aat tcc agt Leu Leu Cys Val Asn Arg Leu Ser Ile Asn Asn Leu Lys Asn Ser Ser 325 330 335			1008

gtt ata att ata gat gaa ata cac gaa cat gat aga tat gct gac ata	1056
Val Ile Ile Ile Asp Glu Ile His Glu His Asp Arg Tyr Ala Asp Ile	
340 345 350	
tgt ata gca gta tca tat ttt tta aaa aaa gtt ata aat atc aga aat	1104
Cys Ile Ala Val Ser Tyr Phe Leu Lys Lys Val Ile Asn Ile Arg Asn	
355 360 365	
ata ata tta ata tct gca aca ata gaa ttt gaa ata gat aat ata tta	1152
Ile Ile Leu Ile Ser Ala Thr Ile Glu Phe Glu Ile Asp Asn Ile Leu	
370 375 380	
aga ttt ttt aat aat aaa ata gta caa gta tat ata cct gga ttt aca	1200
Arg Phe Phe Asn Asn Lys Ile Val Gln Val Tyr Ile Pro Gly Phe Thr	
385 390 395 400	
tta ttt cct gtt aca gaa ata gaa aat acg gtt gat agt ata gat aaa	1248
Leu Phe Pro Val Thr Glu Ile Glu Asn Thr Val Asp Ser Ile Asp Lys	
405 410 415	
ata tta tta gat aat aaa cca cct gtt gga tat tct gtt ata ata ttt	1296
Ile Leu Leu Asp Asn Lys Pro Pro Val Gly Tyr Ser Val Ile Ile Phe	
420 425 430	
tat gaa tca ata cca aaa tta act ttt att aaa aaa aaa tta gaa gaa	1344
Tyr Glu Ser Ile Pro Lys Leu Thr Phe Ile Lys Lys Lys Leu Glu Glu	
435 440 445	
agt ata aaa gat cct ata tat aaa ttt tat tct ata cac gga aaa aca	1392
Ser Ile Lys Asp Pro Ile Tyr Lys Phe Tyr Ser Ile His Gly Lys Thr	
450 455 460	
gat aat gct aat gaa gtt att cgt tat ata gaa aat aat aaa aaa cat	1440
Asp Asn Ala Asn Glu Val Ile Arg Tyr Ile Glu Asn Asn Lys Lys His	
465 470 475 480	
att cat gtc ata ata agt aca aat tat tta gaa tca tct ata act ata	1488
Ile His Val Ile Ile Ser Thr Asn Tyr Leu Glu Ser Ser Ile Thr Ile	
485 490 495	
tcg aat gct aaa tta gta ata gat aat gga aaa gta tat aga aaa gaa	1536
Ser Asn Ala Lys Leu Val Ile Asp Asn Gly Lys Val Tyr Arg Lys Glu	
500 505 510	
ttt ata gat gga aat ata aca tat ata aca aat agt atg tat aaa caa	1584
Phe Ile Asp Gly Asn Ile Thr Tyr Ile Thr Asn Ser Met Tyr Lys Gln	
515 520 525	
aga aaa ggt aga gta gga aga gtg tca aaa gga aca tat ata aga aca	1632
Arg Lys Gly Arg Val Gly Arg Val Ser Lys Gly Thr Tyr Ile Arg Thr	
530 535 540	
tac aca tta gat aaa tta aat act aat ttt aaa aat ata aat tat caa	1680
Tyr Thr Leu Asp Lys Leu Asn Thr Asn Phe Lys Asn Ile Asn Tyr Gln	
545 550 555 560	

tat tta tgg gat tac ata ata att ttt aaa tat tat ggt tta gat ata	1728
Tyr Leu Trp Asp Tyr Ile Ile Ile Phe Lys Tyr Tyr Gly Leu Asp Ile	
565 570 575	
aaa aaa gat tat ttt gta att cct gat aat att aat aga gta gat aaa	1776
Lys Lys Asp Tyr Phe Val Ile Pro Asp Asn Ile Asn Arg Val Asp Lys	
580 585 590	
act gtt aat tat atg aag tct ata gga ata gat ata gat aaa tgt ata	1824
Thr Val Asn Tyr Met Lys Ser Ile Gly Ile Asp Ile Asp Lys Cys Ile	
595 600 605	
aat aaa ata tat aga att ttt aat aaa tat gaa att aat atg tta gaa	1872
Asn Lys Ile Tyr Arg Ile Phe Asn Lys Tyr Glu Ile Asn Met Leu Glu	
610 615 620	
tat ttt att ata tat ttg tat ggt tca gaa act gag aaa tta tta ttg	1920
Tyr Phe Ile Ile Tyr Leu Tyr Gly Ser Glu Thr Glu Lys Leu Leu Leu	
625 630 635 640	
agc aca gat gat aaa aat ata att gat ata cct tat aaa ata tat aat	1968
Ser Thr Asp Asp Lys Asn Ile Ile Asp Ile Pro Tyr Lys Ile Tyr Asn	
645 650 655	
ata tat gta aaa atg aat gta aaa ata aaa ttg gaa tct aaa aga agt	2016
Ile Tyr Val Lys Met Asn Val Lys Ile Lys Leu Glu Ser Lys Arg Ser	
660 665 670	
att ata tat ata ttt aaa ttt att aat gat gta tat gat ggt ccg caa	2064
Ile Ile Tyr Ile Phe Lys Phe Ile Asn Asp Val Tyr Asp Gly Pro Gln	
675 680 685	
aaa ttt aaa tat att aat aca gac gaa aat gta tat ttt gat aaa aat	2112
Lys Phe Lys Tyr Ile Asn Thr Asp Glu Asn Val Tyr Phe Asp Lys Asn	
690 695 700	
aaa ata tat tat tta aaa tct gaa aat cca ctg att att atg aga gat	2160
Lys Ile Tyr Tyr Leu Lys Ser Glu Asn Pro Leu Ile Ile Met Arg Asp	
705 710 715 720	
taa	2163

&lt;210&gt; 39

&lt;211&gt; 813

&lt;212&gt; DNA

&lt;213&gt; Amsacta moorei entomopoxvirus

&lt;220&gt;

&lt;221&gt; exon

&lt;222&gt; (1) .. (813)

&lt;223&gt;

&lt;400&gt; 39

atg tat ata caa ata cca gaa tat aaa aag tca tat atg tgt aaa agt	48
Met Tyr Ile Gln Ile Pro Glu Tyr Lys Lys Ser Tyr Met Cys Lys Ser	
1 5 10 15	
tta ata aac tct gga aca tac gga att gta tat aaa tat gca gat att	96
Leu Ile Asn Ser Gly Thr Tyr Gly Ile Val Tyr Lys Tyr Ala Asp Ile	
20 25 30	
tat aca aaa aat aat gtt gcg att aaa ttt ttt aga aat aat gat aat	144
Tyr Thr Lys Asn Asn Val Ala Ile Lys Phe Phe Arg Asn Asn Asp Asn	
35 40 45	
ttt aca cac gaa ata aat att tta aat tat att aaa aaa aaa ata tat	192
Phe Thr His Glu Ile Asn Ile Leu Asn Tyr Ile Lys Lys Lys Ile Tyr	
50 55 60	
aat aat tct gat agt gat gaa ata aac gaa gtt aaa aaa aat atc tgt	240
Asn Asn Ser Asp Ser Asp Glu Ile Asn Glu Val Lys Lys Asn Ile Cys	
65 70 75 80	
ttt ccg ata ttt ttt aca aat gaa aat aat gtt tca aaa tat att ata	288
Phe Pro Ile Phe Phe Thr Asn Glu Asn Asn Val Ser Lys Tyr Ile Ile	
85 90 95	
ttt aat tat tat gat tat gat tta tta tat tac gca tct aca tat ata	336
Phe Asn Tyr Tyr Asp Tyr Asp Leu Leu Tyr Tyr Ala Ser Thr Tyr Ile	
100 105 110	
tta ctt aat caa gat ata tta aat ata agt tta caa ata tgc aat gga	384
Leu Leu Asn Gln Asp Ile Leu Asn Ile Ser Leu Gln Ile Cys Asn Gly	
115 120 125	
ctg aaa tat tta cat aaa aat tct att gtt cat tgt gat tta aaa cca	432
Leu Lys Tyr Leu His Lys Asn Ser Ile Val His Cys Asp Leu Lys Pro	
130 135 140	
gag aat ata tta tgt aaa tat aaa aat gat aca ttg cat ctt gtt ata	480
Glu Asn Ile Leu Cys Lys Tyr Lys Asn Asp Thr Leu His Leu Val Ile	
145 150 155 160	
aca gat ttt gga tta tcg tat ata gaa aat aat att att gat tat gaa	528
Thr Asp Phe Gly Leu Ser Tyr Ile Glu Asn Asn Ile Ile Asp Tyr Glu	
165 170 175	
atc gta aca ttt agt tat aga tct cct gaa tta ata tgt act att aat	576
Ile Val Thr Phe Ser Tyr Arg Ser Pro Glu Leu Ile Cys Thr Ile Asn	
180 185 190	
aat aaa aac aat ata att gta aag tct tct ata gat atg tgg tct ttt	624
Asn Lys Asn Asn Ile Ile Val Lys Ser Ser Ile Asp Met Trp Ser Phe	

195	200	205	
ggg gta att ata tat ttt tta att aat aaa ttt tat ttt gat att tat			672
Gly Val Ile Ile Tyr Phe Leu Ile Asn Lys Phe Tyr Phe Asp Ile Tyr			
210	215	220	
aat att gaa aaa tat ata gaa tct aat cct ata aaa aaa tta tgt aac			720
Asn Ile Glu Lys Tyr Ile Glu Ser Asn Pro Ile Lys Lys Leu Cys Asn			
225	230	235	240
att aac tcg att gtt gat aga ctg cta caa tat gaa aaa gat aga tat			768
Ile Asn Ser Ile Val Asp Arg Leu Leu Gln Tyr Glu Lys Asp Arg Tyr			
245	250	255	
aca agt tat caa ata tat aat gat ctg aaa aaa tta ttg aaa taa			813
Thr Ser Tyr Gln Ile Tyr Asn Asp Leu Lys Lys Leu Leu Lys			
260	265	270	

&lt;210&gt; 40

&lt;211&gt; 2181

&lt;212&gt; DNA

&lt;213&gt; Amsacta moorei entomopoxvirus

&lt;220&gt;

&lt;221&gt; exon

&lt;222&gt; (1) .. (2181)

&lt;223&gt;

&lt;400&gt; 40

atg tca gac gaa tat ata tat tta cag aaa tct tta aat gtt act aaa			48
Met Ser Asp Glu Tyr Ile Tyr Leu Gln Lys Ser Leu Asn Val Thr Lys			
1	5	10	15
gaa tct aaa ata gat tta ata tta aat gat aaa act agt aaa gat tta			96
Glu Ser Lys Ile Asp Leu Ile Leu Asn Asp Lys Thr Ser Lys Asp Leu			
20	25	30	
gtt aaa ata agt ata tcc aaa ata tgt aga agt att tta aaa tat aaa			144
Val Lys Ile Ser Ile Ser Lys Ile Cys Arg Ser Ile Leu Lys Tyr Lys			
35	40	45	
gat agc aat caa cct att tct gaa tat cat gaa ttt ata ctt gat gat			192
Asp Ser Asn Gln Pro Ile Ser Glu Tyr His Glu Phe Ile Leu Asp Asp			
50	55	60	
att act gat tat ttt aaa tta ttt ttt gat ata gat tgt aaa aca gaa			240



Ile Thr Asp Tyr Phe Lys Leu Phe Phe Asp Ile Asp Cys Lys Thr Glu 65 70 75 80	
tat gaa atc gat gat gtt aaa aaa tat att aaa gaa ttt aaa aaa ttt Tyr Glu Ile Asp Asp Val Lys Lys Tyr Ile Lys Glu Phe Lys Lys Phe 85 90 95	288
ata tca tat gaa ttg tat aat ata ttt tct aat aat ttt gat ata gag Ile Ser Tyr Glu Leu Tyr Asn Ile Phe Ser Asn Asn Phe Asp Ile Glu 100 105 110	336
aat cat aac atc gat aat ata aaa aaa ttt ata ttt aat aat att tac Asn His Asn Ile Asp Asn Ile Lys Lys Phe Ile Phe Asn Asn Ile Tyr 115 120 125	384
tat aca tta tct gat aat ccg cac aaa tta tct tta cat ata ttt ttt Tyr Thr Leu Ser Asp Asn Pro His Lys Leu Ser Leu His Ile Phe Phe 130 135 140	432
aat caa ata tta gta agt cct aca tca ttt ata caa tta aag aaa tat Asn Gln Ile Leu Val Ser Pro Thr Ser Phe Ile Gln Leu Lys Lys Tyr 145 150 155 160	480
ata ata aat tta aga tca aaa ata aat aat att tta atc aat aat ata Ile Ile Asn Leu Arg Ser Lys Ile Asn Asn Ile Leu Ile Asn Asn Ile 165 170 175	528
gat tta gct cct ttt aga aga aat aca caa tta aga ttt ata tat agt Asp Leu Ala Pro Phe Arg Arg Asn Thr Gln Leu Arg Phe Ile Tyr Ser 180 185 190	576
aag aaa aat gat agt gaa tat ttt cac tca gag cat gat tat aat ata Lys Lys Asn Asp Ser Glu Tyr Phe His Ser Glu His Asp Tyr Asn Ile 195 200 205	624
gaa aat ata gaa gat tta aaa aaa tat ata ata aca tat aaa aat ttt Glu Asn Ile Glu Asp Leu Lys Lys Tyr Ile Ile Thr Tyr Lys Asn Phe 210 215 220	672
aat gaa cca cat att ata ata aaa gca aaa gat aat aat tta aca aat Asn Glu Pro His Ile Ile Ile Lys Ala Lys Asp Asn Asn Leu Thr Asn 225 230 235 240	720
ctt gat gta att tat cct cat att aaa tat ttt aga ggt cct cat ttt Leu Asp Val Ile Tyr Pro His Ile Lys Tyr Phe Arg Gly Pro His Phe 245 250 255	768
att aga aat att tct aaa gaa tta tat aat aat tat aaa att aca att Ile Arg Asn Ile Ser Lys Glu Leu Tyr Asn Asn Tyr Lys Ile Thr Ile 260 265 270	816
tct gat gat tca att cag tta ttt aaa aaa aaa cat agc gct gaa tta Ser Asp Asp Ser Ile Gln Leu Phe Lys Lys Lys His Ser Ala Glu Leu 275 280 285	864
gac gaa att att gat ata aat ttg ata ttt aat act cct gat tgt aaa Asp Glu Ile Ile Asp Ile Asn Leu Ile Phe Asn Thr Pro Asp Cys Lys	912

290	295	300	
ata tgt ggt aaa aat tct tta cat aaa aat aat aga att ata aaa ttt Ile Cys Gly Lys Asn Ser Leu His Lys Asn Asn Arg Ile Ile Lys Phe 305 310 315 320			960
aca gaa caa aaa ata att tta ttt aag agt gga aat cca aga aat tgt Thr Glu Gln Lys Ile Ile Leu Phe Lys Ser Gly Asn Pro Arg Asn Cys 325 330 335			1008
aat aca tta aaa tat gat tat cct acg tta tca gga tat gaa ttg gct Asn Thr Leu Lys Tyr Asp Tyr Pro Thr Leu Ser Gly Tyr Glu Leu Ala 340 345 350			1056
aat ttt ata aga gat tta aat att att aaa aag ata gat tct gat gca Asn Phe Ile Arg Asp Leu Asn Ile Ile Lys Lys Ile Asp Ser Asp Ala 355 360 365			1104
tat gtt tat tgg aaa aat gga aaa tgg gca atc gtt gat aat cct tat Tyr Val Tyr Trp Lys Asn Gly Lys Trp Ala Ile Val Asp Asn Pro Tyr 370 375 380			1152
att ttt caa gga ata agt aat atg ata tta gaa aaa tac aga aac aat Ile Phe Gln Gly Ile Ser Asn Met Ile Leu Glu Lys Tyr Arg Asn Asn 385 390 395 400			1200
atg tta ata caa gat ata gat tat att ata aaa aaa ttt ttt gga gaa Met Leu Ile Gln Asp Ile Asp Tyr Ile Ile Lys Lys Phe Phe Gly Glu 405 410 415			1248
gca aaa aat aga ata agt gct aac tta tct atg aat aca gat att att Ala Lys Asn Arg Ile Ser Ala Asn Leu Ser Met Asn Thr Asp Ile Ile 420 425 430			1296
tgt ttt aat cct tat att ata caa ttt aat aat gga gta tat gat tta Cys Phe Asn Pro Tyr Ile Ile Gln Phe Asn Asn Gly Val Tyr Asp Leu 435 440 445			1344
aaa gaa tct aaa ttt tat act ggc gag aat gca aaa aaa tat att cgt Lys Glu Ser Lys Phe Tyr Thr Gly Glu Asn Ala Lys Lys Tyr Ile Arg 450 455 460			1392
cta aac tat att aaa att gat tat aaa gat ata gaa gat atg tct gat Leu Asn Tyr Ile Lys Ile Asp Tyr Lys Asp Ile Glu Asp Met Ser Asp 465 470 475 480			1440
gaa gaa aaa att aaa ttt gaa aat aat tat aat att ctt tta aaa tta Glu Glu Lys Ile Lys Phe Glu Asn Asn Tyr Asn Ile Leu Leu Lys Leu 485 490 495			1488
ttt aat tta gtt att ccc aaa tct aat cct aaa agg ata gtt ttt gaa Phe Asn Leu Val Ile Pro Lys Ser Asn Pro Lys Arg Ile Val Phe Glu 500 505 510			1536
act aat tta tcg tct gtg tta cat tat tgt cat aaa agt gtt ata aca Thr Asn Leu Ser Ser Val Leu His Tyr Cys His Lys Ser Val Ile Thr 515 520 525			1584

ata tta tat ggt cca act tct gga ggt aaa tct act att aaa tat tta	1632
Ile Leu Tyr Gly Pro Thr Ser Gly Gly Lys Ser Thr Ile Lys Tyr Leu	
530 535 540	
tta aga caa tta ttg ttt gac atg ttt tta gaa cct cct ata gaa ttt	1680
Leu Arg Gln Leu Leu Phe Asp Met Phe Leu Glu Pro Pro Ile Glu Phe	
545 550 555 560	
tat caa aat tat att cca aaa aat tca ccc aac tct tgg tta ggt aaa	1728
Tyr Gln Asn Tyr Ile Pro Lys Asn Ser Pro Asn Ser Trp Leu Gly Lys	
565 570 575	
gta gaa gat aaa tta gtt tct ttt gct tgc gaa ggt gat gtt aat cga	1776
Val Glu Asp Lys Leu Val Ser Phe Ala Ser Glu Gly Asp Val Asn Arg	
580 585 590	
aat gaa gta ttt cta aac aaa aat ata aaa caa tat aca gaa caa tat	1824
Asn Glu Val Phe Leu Asn Lys Asn Ile Lys Gln Tyr Thr Glu Gln Tyr	
595 600 605	
att tta ggt aga gat tta aat aaa tct aaa tgt gtt cac aaa aat aca	1872
Ile Leu Gly Arg Asp Leu Asn Lys Ser Lys Cys Val His Lys Asn Thr	
610 615 620	
tta aca caa ttt ata gat tta aat cca aaa cct atg ttt agt tca gta	1920
Leu Thr Gln Phe Ile Asp Leu Asn Pro Lys Pro Met Phe Ser Ser Val	
625 630 635 640	
gat cct gct ttg gtc aaa cgt att gca gtt ata gaa ata aat gag acg	1968
Asp Pro Ala Leu Val Lys Arg Ile Ala Val Ile Glu Ile Asn Glu Thr	
645 650 655	
caa ttc gtc aat gaa aaa tta tca cga gat act gtc aat ata aca tca	2016
Gln Phe Val Asn Glu Lys Leu Ser Arg Asp Thr Val Asn Ile Thr Ser	
660 665 670	
gat aat aga aat ata gta ata gca gat tct acg ttt gac gat aaa att	2064
Asp Asn Arg Asn Ile Val Ile Ala Asp Ser Thr Phe Asp Asp Lys Ile	
675 680 685	
tta aat aat gaa ttt acg cta ccg tta ttt tat att ctg aag aaa tgg	2112
Leu Asn Asn Glu Phe Thr Leu Pro Leu Phe Tyr Ile Leu Lys Lys Trp	
690 695 700	
tct aaa aaa tac cat aaa gat act gtc aaa tta tta tac acc cct gac	2160
Ser Lys Lys Tyr His Lys Asp Thr Val Lys Leu Leu Tyr Thr Pro Asp	
705 710 715 720	
ttt ttt gat aaa caa aat tga	2181
Phe Phe Asp Lys Gln Asn	
725	

&lt;210&gt; 41

&lt;211&gt; 1885

&lt;212&gt; DNA

&lt;213&gt; Amsacta moorei entomopoxvirus

&lt;220&gt;

&lt;221&gt; exon

&lt;222&gt; (1)..(1885)

&lt;223&gt;

&lt;400&gt; 41

atg gaa gaa tta tat tca tta ata aac tac gca tat tct aat gat att	48
Met Glu Glu Leu Tyr Ser Leu Ile Asn Tyr Ala Tyr Ser Asn Asp Ile	
1 5 10 15	
aaa aga aca ata gta aat ttt aga ttt tcg att gat aat aaa ata tat	96
Lys Arg Thr Ile Val Asn Phe Arg Phe Ser Ile Asp Asn Lys Ile Tyr	
20 25 30	
aaa aat tta ttt tct aat ttt cgc gaa gat ata ata att aat aat gaa	144
Lys Asn Leu Phe Ser Asn Phe Arg Glu Asp Ile Ile Ile Asn Asn Glu	
35 40 45	
tat tct agt act aaa ctt aat aat att aaa aac ata gta gaa gtt aga	192
Tyr Ser Ser Thr Lys Leu Asn Asn Ile Lys Asn Ile Val Glu Val Arg	
50 55 60	
tgt tgt tat aaa aat aaa aat ata att aat tta tcg ttg ata aat ccc	240
Cys Cys Tyr Lys Asn Lys Asn Ile Ile Asn Leu Ser Leu Ile Asn Pro	
65 70 75 80	
gaa ata tat aaa aat att att aat ata aat aat aaa aat aat aaa aaa	288
Glu Ile Tyr Lys Asn Ile Ile Asn Ile Asn Asn Lys Asn Asn Lys Lys	
85 90 95	
aaa tgc att aat att aat gcc att aaa gaa aat gaa aat aca caa tat	336
Lys Cys Ile Asn Ile Asn Ala Ile Lys Glu Asn Glu Asn Thr Gln Tyr	
100 105 110	
ctt aaa tat tat tta aat aat tgc aat act agt ttt gat tct ttt att	384
Leu Lys Tyr Tyr Leu Asn Asn Cys Asn Thr Ser Phe Asp Ser Phe Ile	
115 120 125	
aaa aaa aaa aaa gaa aag aag aaa act tta ata aag tta ttt aat aat	432
Lys Lys Lys Lys Glu Lys Lys Lys Thr Leu Ile Lys Leu Phe Asn Asn	
130 135 140	
gat aat gtg cat aat ata tca aat aac act aat cat act aga tat tat	480
Asp Asn Val His Asn Ile Ser Asn Asn Thr Asn His Thr Arg Tyr Tyr	

145	150	155	160	
gaa ata gag tct	gaa tat aat aac tta	aca tca gag gtt	aca ata aaa	528
Glu Ile Glu Ser	Glu Tyr Asn Asn Leu	Thr Ser Glu Val	Thr Ile Lys	
	165	170	175	
tat aaa ata ata	tta gaa ata att aat	gaa aaa att att	act gaa ggt	576
Tyr Lys Ile Ile	Leu Glu Ile Ile	Asn Glu Lys Ile	Ile Ile Thr Glu	
	180	185	190	
aga tta tta tta	cca aat tct att agt	ata act gtt tca	aat aga tca	624
Arg Leu Leu Leu	Pro Asn Ser Ile	Ser Ile Thr Val	Ser Asn Arg Ser	
	195	200	205	
aga att ata tta	tat gat aat aat aaa	ata cag ata ata	tta tca aaa	672
Arg Ile Ile Leu	Tyr Asp Asn Asn Lys	Ile Gln Ile Ile	Leu Ser Lys	
	210	215	220	
gat aaa tca gaa	aat aat atg caa	gat ttt aat aat	ata tgt tct aat	720
Asp Lys Ser Glu	Asn Asn Met Gln	Asp Phe Asn Asn	Ile Cys Ser Asn	
	225	230	235	240
ata tta aaa aca	ttc ttc tct ata	aca aaa gaa tac	aca aat aat gaa	768
Ile Leu Lys Thr	Phe Phe Ser Ile	Thr Lys Glu Tyr	Thr Asn Asn Glu	
	245	250	255	
ata aac gaa aaa	cac ata aaa tcg	ctt agt ata cat	tgt gat ttt aat	816
Ile Asn Glu Lys	His Ile Lys Ser	Leu Ser Ile His	Cys Asp Phe Asn	
	260	265	270	
tat act aat agt	ata tta aaa tac	cca ata ttt ttt	gaa gat aaa aaa	864
Tyr Thr Asn Ser	Ile Leu Lys Tyr	Pro Ile Phe Phe	Glu Asp Lys Lys	
	275	280	285	
ata agg ttt ttt	gga aaa aat aaa	att agt ata aaa	tcc ata aca tca	912
Ile Arg Phe Phe	Gly Lys Asn Lys	Ile Ser Ile Lys	Ser Ile Thr Ser	
	290	295	300	
aaa tct aaa tta	gag aaa att tac	aca tat ata gaa	aaa aat ata tgt	960
Lys Ser Lys Leu	Glu Lys Ile Tyr	Thr Tyr Ile Glu	Lys Asn Ile Cys	
	305	310	315	320
aat ata caa aaa	ttg tat gat gat	ata gat aat tgt	gat ccg ata aat	1008
Asn Ile Gln Lys	Leu Tyr Asp Asp	Ile Asp Asn Cys	Asp Pro Ile Asn	
	325	330	335	
gat ccc att gat	gat ata aat aca	cta gta aat aaa	ata tat ttc aat	1056
Asp Pro Ile Asp	Asp Ile Asn Thr	Leu Val Asn Lys	Ile Tyr Phe Asn	
	340	345	350	
aat tta ttg aaa	taa aat aaa tta	ata tta aat tat	aat gga ttt aat	1104
Asn Leu Leu Lys	Asn Lys Leu Ile	Leu Asn Tyr Asn	Gly Phe Asn	
	355	360	365	
aga ata cga caa	taa tca tta tat	tga acc tat tgc	taa tag aaa aga	1152
Arg Ile Arg Gln	Ser Leu Tyr	Thr Tyr Cys	Lys Arg	
	370	375		

tat ata tct aaa ttt tgt aac agc gcc ttt ggt gca aga tat aga ttg	1200
Tyr Ile Ser Lys Phe Cys Asn Ser Ala Phe Gly Ala Arg Tyr Arg Leu	
380 385 390 395	
ttc att aat aaa aca tga gga taa tat tta tga tgt tac taa ata ttt	1248
Phe Ile Asn Lys Thr Gly Tyr Leu Cys Tyr Ile Phe	
400 405	
tgt att taa aac ata caa tta cga aga tat ata tat agt tta tga tgt	1296
Cys Ile Asn Ile Gln Leu Arg Arg Tyr Ile Tyr Ser Leu Cys	
410 415 420	
gtt att aaa caa agt tgt att att taa att taa ttt tac aat aaa aga	1344
Val Ile Lys Gln Ser Cys Ile Ile Ile Phe Tyr Asn Lys Arg	
425 430 435	
ata tat aat tat aaa taa ttt ttt aat aat aat tta taa tga caa cga	1392
Ile Tyr Asn Tyr Lys Phe Phe Asn Asn Asn Leu Gln Arg	
440 445	
taa cat aat aat tga tat cga aga taa aaa ata tat aaa att taa aaa	1440
His Asn Asn Tyr Arg Arg Lys Ile Tyr Lys Ile Lys	
450 455 460	
atg gaa atc ttt att act aaa ttg tac aca aat agc taa tta tat taa	1488
Met Glu Ile Phe Ile Thr Lys Leu Tyr Thr Asn Ser Leu Tyr	
465 470	
att aat aga aga tga aaa taa aaa aat att tgt taa ata tat aac aaa	1536
Ile Asn Arg Arg Lys Lys Asn Ile Cys Ile Tyr Asn Lys	
475 480 485	
aaa tga tat ttt aat aga taa taa tac tat tga taa taa taa aat aaa	1584
Lys Tyr Phe Asn Arg Tyr Tyr Asn Lys	
490 495	
aaa ata taa taa aat aaa atg tat taa tat aga aaa taa agt tac att	1632
Lys Ile Asn Lys Met Tyr Tyr Arg Lys Ser Tyr Ile	
500 505	
atc aat att aga caa taa taa tga att ata tat aaa taa taa att att	1680
Ile Asn Ile Arg Gln Ile Ile Tyr Lys Ile Ile	
510 515	
taa gct aga tta caa tat ata taa tat att taa ttt ttc gtt aaa aca	1728
Ala Arg Leu Gln Tyr Ile Tyr Ile Phe Phe Val Lys Thr	
520 525 530	
tgt att att att aac aga tat aga cga tgg aaa tat tat aat ttt aaa	1776
Cys Ile Ile Ile Asn Arg Tyr Arg Arg Trp Lys Tyr Tyr Asn Phe Lys	
535 540 545	
ttt aga aaa ttt aga aca aga tga ata caa aaa tta tta tga tat aat	1824
Phe Arg Lys Phe Arg Thr Arg Ile Gln Lys Leu Leu Tyr Asn	
550 555 560	

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agt aat gat aaa tga taa gtt tta taa taa tat cag aaa cgc att ttt      1872
Ser Asn Asp Lys          Val Leu          Tyr Gln Lys Arg Ile Phe
          565                      570

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agt taa tga tta a                      1885
Ser          Leu
575

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<210> 42

<211> 789

<212> DNA

<213> Amsacta moorei entomopoxvirus

<220>

<221> exon

<222> (1) .. (789)

<223>

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<400> 42
atg ctc gat ata acc aaa tct att ata tct tcg ggt ata aat ata aaa      48
Met Leu Asp Ile Thr Lys Ser Ile Ile Ser Ser Gly Ile Asn Ile Lys
1          5          10          15

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tta cca agt gtt aac ata ata caa aat ata aaa cca aaa tat tat aat      96
Leu Pro Ser Val Asn Ile Ile Gln Asn Ile Lys Pro Lys Tyr Tyr Asn
          20          25          30

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aat agt tct ccc aaa tca tat ttt ggg att ata tat cat tta ttg tca      144
Asn Ser Ser Pro Lys Ser Tyr Phe Gly Ile Ile Tyr His Leu Leu Ser
          35          40          45

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ata gtt ata gaa ata caa gac aca tat aaa tta aat gat aat ata gga      192
Ile Val Ile Glu Ile Gln Asp Thr Tyr Lys Leu Asn Asp Asn Ile Gly
          50          55          60

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tat ttt aca aaa tat gat gat atg aag aaa aaa aat aaa aca gat tac      240
Tyr Phe Thr Lys Tyr Asp Asp Met Lys Lys Lys Asn Lys Thr Asp Tyr
65          70          75          80

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gat tat tct tat aat aat ctt ttt aaa aca gat att aaa tta gaa aaa      288
Asp Tyr Ser Tyr Asn Asn Leu Phe Lys Thr Asp Ile Lys Leu Glu Lys
          85          90          95

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agt ggt tca tcg atg aag aat tgg aca aat ata tat aat aca aca gat      336
Ser Gly Ser Ser Met Lys Asn Trp Thr Asn Ile Tyr Asn Thr Thr Asp
          100          105          110

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gtt act att gat ata tta aat ccg tta aat aaa aaa cac gat aaa cta      384
Val Thr Ile Asp Ile Leu Asn Pro Leu Asn Lys Lys His Asp Lys Leu
      115                      120                      125

tct ata aga tta cct tgt gta ata tct aca tct gtt ata cat tat tta      432
Ser Ile Arg Leu Pro Cys Val Ile Ser Thr Ser Val Ile His Tyr Leu
      130                      135                      140

tat att tta tca tat att tat gaa tca gtt aca tta ata aaa gaa gat      480
Tyr Ile Leu Ser Tyr Ile Tyr Glu Ser Val Thr Leu Ile Lys Glu Asp
      145                      150                      155                      160

ttg tgg tta aac gat agt ttt ata gtt aaa tgt gaa aat tta aga aca      528
Leu Trp Leu Asn Asp Ser Phe Ile Val Lys Cys Glu Asn Leu Arg Thr
      165                      170                      175

aat aat tat aat aat gta aaa tcg cag tta aaa aca att gta ttt aat      576
Asn Asn Tyr Asn Asn Val Lys Ser Gln Leu Lys Thr Ile Val Phe Asn
      180                      185                      190

gaa aaa aca aga caa tat aaa ata gac gga tta ttt aaa aat ttc ata      624
Glu Lys Thr Arg Gln Tyr Lys Ile Asp Gly Leu Phe Lys Asn Phe Ile
      195                      200                      205

ata gac gaa agt ttt aaa aat ata ata agt aaa ttt att aat gat att      672
Ile Asp Glu Ser Phe Lys Asn Ile Ile Ser Lys Phe Ile Asn Asp Ile
      210                      215                      220

caa tgt gtt ata tgc gat cta tgg tta act att caa aaa aat ata aat      720
Gln Cys Val Ile Cys Asp Leu Trp Leu Thr Ile Gln Lys Asn Ile Asn
      225                      230                      235                      240

gat tca cca tct gat aga aaa aaa att tat tgg gaa gaa tat gat aat      768
Asp Ser Pro Ser Asp Arg Lys Lys Ile Tyr Trp Glu Glu Tyr Asp Asn
      245                      250                      255

att ttg gga ttt caa aat tga      789
Ile Leu Gly Phe Gln Asn
      260

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<210> 43

<211> 2304

<212> DNA

<213> Amsacta moorei entomopoxvirus

<220>

<221> exon



&lt;222&gt; (1) .. (2304)

&lt;223&gt;

&lt;400&gt; 43

atg gat ata aca gat aat agt tat gaa tat tcg aca ata aac cca caa	48
Met Asp Ile Thr Asp Asn Ser Tyr Glu Tyr Ser Thr Ile Asn Pro Gln	
1 5 10 15	
ggt ata ttt tta ttt gat gaa aac aag aat gtt aaa aag aca ata ttt	96
Val Ile Phe Leu Phe Asp Glu Asn Lys Asn Val Lys Lys Thr Ile Phe	
20 25 30	
tta tct aaa gat agt ata ata gat aat agt ttt gca tat gga gta tat	144
Leu Ser Lys Asp Ser Ile Ile Asp Asn Ser Phe Ala Tyr Gly Val Tyr	
35 40 45	
aat tat tta tta tct aca aat aca aaa ttt cta tca caa cca gaa tat	192
Asn Tyr Leu Leu Ser Thr Asn Thr Lys Phe Leu Ser Gln Pro Glu Tyr	
50 55 60	
att aat gat cat gtt ata tta tca ttc aat ctt gaa caa gct aga gga	240
Ile Asn Asp His Val Ile Leu Ser Phe Asn Leu Glu Gln Ala Arg Gly	
65 70 75 80	
tac att aga aat ata tta aga att aac gaa aat att att tta ttt tca	288
Tyr Ile Arg Asn Ile Leu Arg Ile Asn Glu Asn Ile Ile Leu Phe Ser	
85 90 95	
ata tgg cat aat tta gat tat tat tat aat aac aat gaa ata ttt gat	336
Ile Trp His Asn Leu Asp Tyr Tyr Tyr Asn Asn Asn Glu Ile Phe Asp	
100 105 110	
cca tat aat ata aaa aat aat tta tta ata gaa tct aat gat aat aaa	384
Pro Tyr Asn Ile Lys Asn Asn Leu Leu Ile Glu Ser Asn Asp Asn Lys	
115 120 125	
aaa ata tta tat atg tta gat att agt att act aat ggt gct ata ttt	432
Lys Ile Leu Tyr Met Leu Asp Ile Ser Ile Thr Asn Gly Ala Ile Phe	
130 135 140	
tgt gtt act act aac agt tat act aat aca aat tta gct aaa gaa ggc	480
Cys Val Thr Thr Asn Ser Tyr Thr Asn Thr Asn Leu Ala Lys Glu Gly	
145 150 155 160	
ata tat tca aaa att tat aca gaa tat ata caa gaa ata ata ttt aat	528
Ile Tyr Ser Lys Ile Tyr Thr Glu Tyr Ile Gln Glu Ile Ile Phe Asn	
165 170 175	
ata tat aaa aat aac tat aaa tta tct tcc gtt gta aaa gaa tca gaa	576
Ile Tyr Lys Asn Asn Tyr Lys Leu Ser Ser Val Val Lys Glu Ser Glu	
180 185 190	
gaa tat tct tta aca aat aat ttt gat gat ata atc aaa tta tca aat	624
Glu Tyr Ser Leu Thr Asn Asn Phe Asp Asp Ile Ile Lys Leu Ser Asn	

195	200	205	
att aat aaa tat aaa aag aca tta tgt att ggc gta tat gat aaa tat			672
Ile Asn Lys Tyr Lys Lys Thr Leu Cys Ile Gly Val Tyr Asp Lys Tyr			
210	215	220	
tat ata aag ggt gat aaa ata tca atc ttg gat aac tac aac gat tca			720
Tyr Ile Lys Gly Asp Lys Ile Ser Ile Leu Asp Asn Tyr Asn Asp Ser			
225	230	235	240
gaa tat aca tca tta tac ata tat ata gat caa aat aat ata ata aaa			768
Glu Tyr Thr Ser Leu Tyr Ile Tyr Ile Asp Gln Asn Asn Ile Ile Lys			
245	250	255	
atc act aat gat gta tta ata aca gaa aaa tta act tat ttt aca gat			816
Ile Thr Asn Asp Val Leu Ile Thr Glu Lys Leu Thr Tyr Phe Thr Asp			
260	265	270	
ata tta aaa gaa gaa gaa ata aaa aat ata att att aaa tca act agt			864
Ile Leu Lys Glu Glu Glu Ile Lys Asn Ile Ile Ile Lys Ser Thr Ser			
275	280	285	
cca aaa agt att ata tat ata tat ttt gat acg ttt tta gac tct aat			912
Pro Lys Ser Ile Ile Tyr Ile Tyr Phe Asp Thr Phe Leu Asp Ser Asn			
290	295	300	
ata aat ata caa tat gat ctt aaa ttt ttt cta aat gtt aca aac act			960
Ile Asn Ile Gln Tyr Asp Leu Lys Phe Phe Leu Asn Val Thr Asn Thr			
305	310	315	320
aga aat ata ttt ata gat atg tct tat aaa att aat att atg aca tct			1008
Arg Asn Ile Phe Ile Asp Met Ser Tyr Lys Ile Asn Ile Met Thr Ser			
325	330	335	
aaa aat cac ata tca ttt aga tct ttt aac ata gat gta aat tta tgt			1056
Lys Asn His Ile Ser Phe Arg Ser Phe Asn Ile Asp Val Asn Leu Cys			
340	345	350	
aaa tat tta tcg tta ttg ata tta gga tat aat cat att ttt aat aaa			1104
Lys Tyr Leu Ser Leu Leu Ile Leu Gly Tyr Asn His Ile Phe Asn Lys			
355	360	365	
ata caa aaa cac gct aga ctt aaa aaa att gat gag ctt tat cct tcg			1152
Ile Gln Lys His Ala Arg Leu Lys Lys Ile Asp Glu Leu Tyr Pro Ser			
370	375	380	
agg tat tgt caa aat tat aaa gat gtt aaa aga caa cct gtt tta ata			1200
Arg Tyr Cys Gln Asn Tyr Lys Asp Val Lys Arg Gln Pro Val Leu Ile			
385	390	395	400
gat tcg ata gat gaa aat tat tta att aaa ata tct gat aaa tat tat			1248
Asp Ser Ile Asp Glu Asn Tyr Leu Ile Lys Ile Ser Asp Lys Tyr Tyr			
405	410	415	
gtg ggt aaa gaa gat act aca agg aca tat caa cac aaa gga act aaa			1296
Val Gly Lys Glu Asp Thr Thr Arg Thr Tyr Gln His Lys Gly Thr Lys			
420	425	430	

aaa ata ttt gat cca tac aaa tac ggt gat gtt tat ata gat gat aat	1344
Lys Ile Phe Asp Pro Tyr Lys Tyr Gly Asp Val Tyr Ile Asp Asp Asn	
435 440 445	
ggt tta ata tat caa tgt tct agt att tat tat tca aat atg gga ttt	1392
Gly Leu Ile Tyr Gln Cys Ser Ser Ile Tyr Tyr Ser Asn Met Gly Phe	
450 455 460	
ttg aat aat ata tat tta gct agt gga gga aaa act tgt tat cct tgt	1440
Leu Asn Asn Ile Tyr Leu Ala Ser Gly Gly Lys Thr Cys Tyr Pro Cys	
465 470 475 480	
tgt tat tca aaa cag aaa aat aga gat gaa ata ttc gaa tct tgc gtt	1488
Cys Tyr Ser Lys Gln Lys Asn Arg Asp Glu Ile Phe Glu Ser Cys Val	
485 490 495	
tat aat aaa gaa att att tta gaa gat aaa ata aat ccc ata ata gtt	1536
Tyr Asn Lys Glu Ile Ile Leu Glu Asp Lys Ile Asn Pro Ile Ile Val	
500 505 510	
aat tat gga aga att ata tta agt aag aat ggt tta tct aaa tta tca	1584
Asn Tyr Gly Arg Ile Ile Leu Ser Lys Asn Gly Leu Ser Lys Leu Ser	
515 520 525	
cct aaa tta aat aat att tta aac gct aat tca aaa ata gat att gtt	1632
Pro Lys Leu Asn Asn Ile Leu Asn Ala Asn Ser Lys Ile Asp Ile Val	
530 535 540	
aaa cat act aat aga ata gat ttt tca gat aat tat aca ata ata atg	1680
Lys His Thr Asn Arg Ile Asp Phe Ser Asp Asn Tyr Thr Ile Ile Met	
545 550 555 560	
tca tat caa cca act att act ata aga aat ttt gat gac atg tat tat	1728
Ser Tyr Gln Pro Thr Ile Thr Ile Arg Asn Phe Asp Asp Met Tyr Tyr	
565 570 575	
ttt att ata aac aat aat gct att gtt att aat gat aat ata gtt tat	1776
Phe Ile Ile Asn Asn Asn Ala Ile Val Ile Asn Asp Asn Ile Val Tyr	
580 585 590	
act gat aaa agt ata tta aaa atg aat aat aat aat ata aat gta ttt	1824
Thr Asp Lys Ser Ile Leu Lys Met Asn Asn Asn Asn Ile Asn Val Phe	
595 600 605	
ata ata ata caa aat aga att cat caa tta aaa aat att gat aaa caa	1872
Ile Ile Ile Gln Asn Arg Ile His Gln Leu Lys Asn Ile Asp Lys Gln	
610 615 620	
tca aaa tat gat gat ata gta gtt aat aaa ata gat gat aaa aaa ata	1920
Ser Lys Tyr Asp Asp Ile Val Val Asn Lys Ile Asp Asp Lys Lys Ile	
625 630 635 640	
aaa ata att aaa aaa tac ttt aat ata ata tcc aat ata cga aat cca	1968
Lys Ile Ile Lys Lys Tyr Phe Asn Ile Ile Ser Asn Ile Arg Asn Pro	
645 650 655	

ata tct aat aat gga att tct ata aca gat gat gtt tgt act ata gat	2016
Ile Ser Asn Asn Gly Ile Ser Ile Thr Asp Asp Val Cys Thr Ile Asp	
660 665 670	

ggc gaa tta ata gaa aat aaa aat att aaa tat ttt tct gaa tat aat	2064
Gly Glu Leu Ile Glu Asn Lys Asn Ile Lys Tyr Phe Ser Glu Tyr Asn	
675 680 685	

aat att tct tta aaa cct aaa agt act agc gaa tat ata gaa aag tat	2112
Asn Ile Ser Leu Lys Pro Lys Ser Thr Ser Glu Tyr Ile Glu Lys Tyr	
690 695 700	

ttt aaa caa tat ttt gat act ata tat act aat aat att aga tta ttt	2160
Phe Lys Gln Tyr Phe Asp Thr Ile Tyr Thr Asn Asn Ile Arg Leu Phe	
705 710 715 720	

ata aaa ata ttt ata acg aaa ata atg cat agt ata aaa gaa aca gac	2208
Ile Lys Ile Phe Ile Thr Lys Ile Met His Ser Ile Lys Glu Thr Asp	
725 730 735	

att ata aaa aca gat tat act aaa tta gaa gaa aaa tta aat aat att	2256
Ile Ile Lys Thr Asp Tyr Thr Lys Leu Glu Glu Lys Leu Asn Asn Ile	
740 745 750	

act aat aaa caa atg tca tct gtt ata ttg tca aaa aaa agt att taa	2304
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<210> 44

<211> 318

<212> DNA

<213> Amsacta moorei entomopoxvirus

<220>

<221> exon

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1 5 10 15	

aga ata tat tat aca att tct act tta aat aaa gaa aat tat ata cat	96
Arg Ile Tyr Tyr Thr Ile Ser Thr Leu Asn Lys Glu Asn Tyr Ile His	
20 25 30	

aat gtt gaa aaa tta aaa tta ata tta tat ttg ata tgt agt aca tta 144  
 Asn Val Glu Lys Leu Lys Leu Ile Leu Tyr Leu Ile Cys Ser Thr Leu  
           35                          40                          45

cca tgc gaa aca tgt gca gct gaa gct aaa aaa aaa ata caa aaa aat 192  
 Pro Cys Glu Thr Cys Ala Ala Glu Ala Lys Lys Lys Ile Gln Lys Asn  
           50                          55                          60

aat ata atg tct gaa tta aat att aat aga att tta cat ttt tat ata 240  
 Asn Ile Met Ser Glu Leu Asn Ile Asn Arg Ile Leu His Phe Tyr Ile  
           65                          70                          75                          80

gaa ttt tat aat ata ttt cat aat aat aaa ata gat aga aaa aaa ata 288  
 Glu Phe Tyr Asn Ile Phe His Asn Asn Lys Ile Asp Arg Lys Lys Ile  
                                   85                          90                          95

aaa aca tat gat act ttt aac tat gta taa 318  
 Lys Thr Tyr Asp Thr Phe Asn Tyr Val  
                   100                          105

<210> 45

<211> 1703

<212> DNA

<213> Amsacta moorei entomopoxvirus

<220>

<221> exon

<222> (1) .. (1703)

<223>

<400> 45  
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 Met Lys Arg Thr Phe Ile Pro Phe Ser Lys Thr Asn Ile Asp Ser Asp  
   1                  5                          10                          15

agg cct aat att tat ata aca gaa act aaa aat ggt aaa tat aac ata 96  
 Arg Pro Asn Ile Tyr Ile Thr Glu Thr Lys Asn Gly Lys Tyr Asn Ile  
           20                          25                          30

cca caa tat gta tca agt cct tgt acg ttt caa gat ggt tat gca gta 144  
 Pro Gln Tyr Val Ser Ser Pro Cys Thr Phe Gln Asp Gly Tyr Ala Val  
           35                          40                          45

gct tct ata aca gat att aaa tta gaa ggc tgt aat aat ttt gga tta 192  
 Ala Ser Ile Thr Asp Ile Lys Leu Glu Gly Cys Asn Asn Phe Gly Leu

50	55	60	
aat ata act ttg cct gaa ata aaa ggt ata ggt ggt gtt agg ttt cag			240
Asn Ile Thr Leu Pro Glu Ile Lys Gly Ile Gly Gly Val Arg Phe Gln			
65	70	75	80
aat tat ttc att cct aaa ctt atc gaa gaa tgt att ata gaa act atc			288
Asn Tyr Phe Ile Pro Lys Leu Ile Glu Glu Cys Ile Ile Glu Thr Ile			
	85	90	95
gat gat aat aaa act aac gaa ata att aga aaa act ggg ctt gaa ttt			336
Asp Asp Asn Lys Thr Asn Glu Ile Ile Arg Lys Thr Gly Leu Glu Phe			
	100	105	110
tta atg gat ttt ata cag aag aaa aaa gaa tat tcg aga ttt gta ggc			384
Leu Met Asp Phe Ile Gln Lys Lys Lys Glu Tyr Ser Arg Phe Val Gly			
	115	120	125
aat aat tct gat tta tgt aaa ttt aaa tat ggt aaa gtg ctg atg ata			432
Asn Asn Ser Asp Leu Cys Lys Phe Lys Tyr Gly Lys Val Leu Met Ile			
	130	135	140
tta ttt ttc cat cta aag aag tat att ttc ctc taa tgt tta tat ttg			480
Leu Phe Phe His Leu Lys Lys Tyr Ile Phe Leu Cys Leu Tyr Leu			
145	150	155	
ata atg tta ata tga atc cca gaa ctt gtt tta gat tat tcc ctg aaa			528
Ile Met Leu Ile Ile Pro Glu Leu Val Leu Asp Tyr Ser Leu Lys			
160	165	170	
cta aat tac aaa taa aaa taa aat tta gac cat ttg cag ata ttt tat			576
Leu Asn Tyr Lys Lys Asn Leu Asp His Leu Gln Ile Phe Tyr			
175	180	185	
tac ccg atg taa aat ata aga aaa ata gtc tta aaa ata ttt cag atg			624
Tyr Pro Met Asn Ile Arg Lys Ile Val Leu Lys Ile Phe Gln Met			
190	195	200	
ttg atc tac aac cat ata taa aat tta ctg gtt ata ata cgt gcg gaa			672
Leu Ile Tyr Asn His Ile Asn Leu Leu Val Ile Ile Arg Ala Glu			
205	210	215	
gtc ctt tta aac ata gat ata tag aag aat taa ctt att cta cac aca			720
Val Leu Leu Asn Ile Asp Ile Lys Asn Leu Ile Leu His Thr			
220	225	230	
aaa gta ata aaa aga att att att cac ctg aat ttt tat cta taa cta			768
Lys Val Ile Lys Arg Ile Ile Ile His Leu Asn Phe Tyr Leu Leu			
235	240	245	
atc tat tat ggt att cta aat ctg ata ttt tca gag gaa ata tgt tta			816
Ile Tyr Tyr Gly Ile Leu Asn Leu Ile Phe Ser Glu Glu Ile Cys Leu			
250	255	260	
tat cat atc ccg att atc cag aaa cag aag aaa att tta tca aaa cat			864
Tyr His Ile Pro Ile Ile Gln Lys Gln Lys Lys Ile Leu Ser Lys His			
265	270	275	

acg ttg ata aat tat taa aag atc ttt taa tta ttt ctg atg atg aaa	912
Thr Leu Ile Asn Tyr Lys Ile Phe Leu Phe Leu Met Met Lys	
280 285 290	
act tta tta aat caa aag gat tta gtg ata aat gta agt tta aaa aaa	960
Thr Leu Leu Asn Gln Lys Asp Leu Val Ile Asn Val Ser Leu Lys Lys	
295 300 305	
ttg atc cgt gtg ata aaa ttg tgt ttg atg tta ata ata att gtg aaa	1008
Leu Ile Arg Val Ile Lys Leu Cys Leu Met Leu Ile Ile Ile Val Lys	
310 315 320 325	
tta ata taa tga atg tcc cgg aag gtt ttg att tat att atc ata caa	1056
Leu Ile Met Ser Arg Lys Val Leu Ile Tyr Ile Ile Ile Gln	
330 335	
ata tat tat cat tca gta gaa gaa ata acc caa atg att ata ata ttt	1104
Ile Tyr Tyr His Ser Val Glu Glu Ile Thr Gln Met Ile Ile Ile Phe	
340 345 350 355	
cta aaa aat tta gta aaa tat ctg gaa cat ata tac cta acg aag ata	1152
Leu Lys Asn Leu Val Lys Tyr Leu Glu His Ile Tyr Leu Thr Lys Ile	
360 365 370	
aga ttt taa tac acg aag taa aac ata caa taa aca tat ctg acg tta	1200
Arg Phe Tyr Thr Lys Asn Ile Gln Thr Tyr Leu Thr Leu	
375 380	
gta ttc cat tga gta tat gga atg caa atg aga ata ctt cta cgg gtg	1248
Val Phe His Val Tyr Gly Met Gln Met Arg Ile Leu Leu Arg Val	
385 390 395	
att tga gat cta tta aat cta aaa aat cag ata tat atg taa atg atc	1296
Ile Asp Leu Leu Asn Leu Lys Asn Gln Ile Tyr Met Met Ile	
400 405 410	
ctt ttg ttt ttg gat tag att ttt tat caa aag aat tag gaa tta tta	1344
Leu Leu Phe Leu Asp Ile Phe Tyr Gln Lys Asn Glu Leu Leu	
415 420 425	
gca gat cta taa caa gta gtt cta atg aat caa tag ctg aat ata aca	1392
Ala Asp Leu Gln Val Val Leu Met Asn Gln Leu Asn Ile Thr	
430 435 440	
gtg ata ccg taa ata ttg aat cat att ttc aat ctg ata att tat ttg	1440
Val Ile Pro Ile Leu Asn His Ile Phe Asn Leu Ile Ile Tyr Leu	
445 450 455	
cag tta cgc caa cat cag aat att caa acc cag caa tat ttt tac ata	1488
Gln Leu Arg Gln His Gln Asn Ile Gln Thr Gln Gln Tyr Phe Tyr Ile	
460 465 470	
gat tta atc ttc ata ata taa ttt tta ttg aac cat cta gat taa tag	1536
Asp Leu Ile Phe Ile Ile Phe Leu Leu Asn His Leu Asp	
475 480 485	

ccg atg ctg cta aaa att tta gat gcg tta att taa gta tag att gga 1584  
 Pro Met Leu Leu Lys Ile Leu Asp Ala Leu Ile Val Ile Gly  
 490 495

aag aat ttc ctg aag tag atc caa gaa gtt tat tta aca aag aat tac 1632  
 Lys Asn Phe Leu Lys Ile Gln Glu Val Tyr Leu Thr Lys Asn Tyr  
 500 505 510

aaa ttt gtc aaa cta ttg tta aaa aaa tat cat atg ata ata ata tta 1680  
 Lys Phe Val Lys Leu Leu Leu Lys Lys Tyr His Met Ile Ile Ile Leu  
 515 520 525 530

taa ccg ttc ata ttc tag agt aa 1703  
 Pro Phe Ile Phe Ser  
 535

<210> 46

<211> 2619

<212> DNA

<213> Amsacta moorei entomopoxvirus

<220>

<221> exon

<222> (1)..(2619)

<223>

<400> 46  
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agt aat att aat ttt gat agt aat cca aat gtt aat aat gaa ata gaa 96  
 Ser Asn Ile Asn Phe Asp Ser Asn Pro Asn Val Asn Asn Glu Ile Glu  
 20 25 30

ttt aca tac ata aat cca gat tta aga att tta tct aat att tat act 144  
 Phe Thr Tyr Ile Asn Pro Asp Leu Arg Ile Leu Ser Asn Ile Tyr Thr  
 35 40 45

gat aat aat gaa tct aaa aaa aaa aca tat tta gaa tat gta ctt aaa 192  
 Asp Asn Asn Glu Ser Lys Lys Lys Thr Tyr Leu Glu Tyr Val Leu Lys  
 50 55 60

ttt gct aac aaa aag tct aaa tta aga caa aaa tat aaa tat gat tat 240  
 Phe Ala Asn Lys Lys Ser Lys Leu Arg Gln Lys Tyr Lys Tyr Asp Tyr  
 65 70 75 80



cct act ttt gaa ata gca aat tca tat ttt tta gat aaa ctt act aat	288
Pro Thr Phe Glu Ile Ala Asn Ser Tyr Phe Leu Asp Lys Leu Thr Asn	
85 90 95	
aat tgg gaa aga aaa act ata ata tca gaa gat aaa ata aat att aat	336
Asn Trp Glu Arg Lys Thr Ile Ile Ser Glu Asp Lys Ile Asn Ile Asn	
100 105 110	
aaa aat gaa tat att tta ttg aga cat aat act gaa tat caa gat aat	384
Lys Asn Glu Tyr Ile Leu Leu Arg His Asn Thr Glu Tyr Gln Asp Asn	
115 120 125	
gat ata gaa tta ccg tta tta aat gat ata ttg gat aaa ata aat gta	432
Asp Ile Glu Leu Pro Leu Leu Asn Asp Ile Leu Asp Lys Ile Asn Val	
130 135 140	
tta ttt gtt tcg caa tta tat ata att ata aat gat tta ata aaa gtt	480
Leu Phe Val Ser Gln Leu Tyr Ile Ile Ile Asn Asp Leu Ile Lys Val	
145 150 155 160	
gaa ttt aaa ata aaa tca aac att gga cca tta tcg tca aat aaa tta	528
Glu Phe Lys Ile Lys Ser Asn Ile Gly Pro Leu Ser Ser Asn Lys Leu	
165 170 175	
tta tta agt aca cat ttc aat gat ata gaa aca tat aga aaa aat ata	576
Leu Leu Ser Thr His Phe Asn Asp Ile Glu Thr Tyr Arg Lys Asn Ile	
180 185 190	
aca tat tat tta gaa ata gaa gta cta tct aaa aca aaa ttg gat aat	624
Thr Tyr Tyr Leu Glu Ile Glu Val Leu Ser Lys Thr Lys Leu Asp Asn	
195 200 205	
aat gta ctt tat gat aat tta gta aaa tct ttt gaa tat ata tat aaa	672
Asn Val Leu Tyr Asp Asn Leu Val Lys Ser Phe Glu Tyr Ile Tyr Lys	
210 215 220	
agc aaa aat ata tct aat ata agt tta gtt aca ata aaa aat aaa cct	720
Ser Lys Asn Ile Ser Asn Ile Ser Leu Val Thr Ile Lys Asn Lys Pro	
225 230 235 240	
aaa ata aaa aca cat atg ata caa tat aat aaa tta aat aca att gat	768
Lys Ile Lys Thr His Met Ile Gln Tyr Asn Lys Leu Asn Thr Ile Asp	
245 250 255	
aaa gaa tca tat att atg gct att aaa att gat gga gat gtt gta gaa	816
Lys Glu Ser Tyr Ile Met Ala Ile Lys Ile Asp Gly Asp Val Val Glu	
260 265 270	
ttt aat gtt atg aat gga att tgt aat atc ata ata tat gat atg gta	864
Phe Asn Val Met Asn Gly Ile Cys Asn Ile Ile Ile Tyr Asp Met Val	
275 280 285	
tat aaa aat ttt tca tgt aac ata gat aaa aat ata caa atg ata ggt	912
Tyr Lys Asn Phe Ser Cys Asn Ile Asp Lys Asn Ile Gln Met Ile Gly	
290 295 300	

atg gga gaa tac att aag gta gat aat gtt aaa aaa ata tat cca ttt	960
Met Gly Glu Tyr Ile Lys Val Asp Asn Val Lys Lys Ile Tyr Pro Phe	
305 310 315 320	
tat ttt tca aaa tta tct tat aat aat aaa aaa ata ata aat aat att	1008
Tyr Phe Ser Lys Leu Ser Tyr Asn Asn Lys Lys Ile Ile Asn Asn Ile	
325 330 335	
cta gat aga tat aag caa ata caa tat tat aat gat aat tta ttg tgt	1056
Leu Asp Arg Tyr Lys Gln Ile Gln Tyr Tyr Asn Asp Asn Leu Leu Cys	
340 345 350	
cat aaa cca aat atg caa att aaa ttt gaa aac aaa tta act tta aaa	1104
His Lys Pro Asn Met Gln Ile Lys Phe Glu Asn Lys Leu Thr Leu Lys	
355 360 365	
ttt gac gaa aat aac gta act aca aat gta cta aaa ttt tat aaa tca	1152
Phe Asp Glu Asn Asn Val Thr Thr Asn Val Leu Lys Phe Tyr Lys Ser	
370 375 380	
ata gaa aat agt tca ttt aaa aat ata tac gat ggt att gta tta cta	1200
Ile Glu Asn Ser Ser Phe Lys Asn Ile Tyr Asp Gly Ile Val Leu Leu	
385 390 395 400	
gat att aca gat aat gat tct aaa aaa gat tat aaa ttt aaa ata gat	1248
Asp Ile Thr Asp Asn Asp Ser Lys Lys Asp Tyr Lys Phe Lys Ile Asp	
405 410 415	
aat act gta gat gtt ata tgt aaa ttg gac act tat aga gga aca tat	1296
Asn Thr Val Asp Val Ile Cys Lys Leu Asp Thr Tyr Arg Gly Thr Tyr	
420 425 430	
ata tta cac aat gat aat aaa tta tat ata act ttt aca tta tat caa	1344
Ile Leu His Asn Asp Asn Lys Leu Tyr Ile Thr Phe Thr Leu Tyr Gln	
435 440 445	
tat gat aat aaa aat ttt aca gaa att tta aaa tac gaa gaa aag aac	1392
Tyr Asp Asn Lys Asn Phe Thr Glu Ile Leu Lys Tyr Glu Glu Lys Asn	
450 455 460	
gaa att ata gaa tat aat aat tat gtt aac tta tta att ttt aat aat	1440
Glu Ile Ile Glu Tyr Asn Asn Tyr Val Asn Leu Leu Ile Phe Asn Asn	
465 470 475 480	
aat aat aaa ttt ggt cct aaa aaa atg tta tcg ccc ata tgg tgt att	1488
Asn Asn Lys Phe Gly Pro Lys Lys Met Leu Ser Pro Ile Trp Cys Ile	
485 490 495	
gta gaa tat tca ttt tta gaa tct aaa att att gga tta aga atc gat	1536
Val Glu Tyr Ser Phe Leu Glu Ser Lys Ile Ile Gly Leu Arg Ile Asp	
500 505 510	
aaa act aat aat ttc tat aga caa aat tat aat ggc aat aat cta gat	1584
Lys Thr Asn Asn Phe Tyr Arg Gln Asn Tyr Asn Gly Asn Asn Leu Asp	
515 520 525	
gtt ata tta aca tcc aaa cac att cac gaa gaa ttt cca tca aat tat	1632

Val	Ile	Leu	Thr	Ser	Lys	His	Ile	His	Glu	Glu	Phe	Pro	Ser	Asn	Tyr	
530						535					540					
aat	att	gat	tat	tta	atg	tct	tta	aat	gaa	act	ata	aat	gta	ata	gat	1680
Asn	Ile	Asp	Tyr	Leu	Met	Ser	Leu	Asn	Glu	Thr	Ile	Asn	Val	Ile	Asp	
545					550					555					560	
aat	aat	cca	cac	aga	tcc	aaa	tta	tta	tta	aat	aaa	gaa	gtt	aat	aaa	1728
Asn	Asn	Pro	His	Arg	Ser	Lys	Leu	Leu	Leu	Asn	Lys	Glu	Val	Asn	Lys	
				565					570					575		
tat	ttt	atg	aat	aat	act	att	aga	aca	tct	ata	aat	ata	tta	aca	aat	1776
Tyr	Phe	Met	Asn	Asn	Thr	Ile	Arg	Thr	Ser	Ile	Asn	Ile	Leu	Thr	Asn	
			580					585					590			
tat	tta	aaa	act	aat	ggg	ata	tcg	atg	gct	ata	tca	aaa	tta	gta	aca	1824
Tyr	Leu	Lys	Thr	Asn	Gly	Ile	Ser	Met	Ala	Ile	Ser	Lys	Leu	Val	Thr	
		595					600					605				
act	tta	cca	aat	aga	tat	gtt	tta	agt	ata	gat	ata	gga	aga	gga	gga	1872
Thr	Leu	Pro	Asn	Arg	Tyr	Val	Leu	Ser	Ile	Asp	Ile	Gly	Arg	Gly	Gly	
	610					615					620					
gat	tta	act	aaa	tat	tat	tat	gtc	gga	ata	aca	gga	atg	tta	gga	aca	1920
Asp	Leu	Thr	Lys	Tyr	Tyr	Tyr	Val	Gly	Ile	Thr	Gly	Met	Leu	Gly	Thr	
625					630					635				640		
gat	cct	gat	att	ttt	gct	ata	aaa	gaa	gca	aga	gat	aga	tat	aaa	aaa	1968
Asp	Pro	Asp	Ile	Phe	Ala	Ile	Lys	Glu	Ala	Arg	Asp	Arg	Tyr	Lys	Lys	
				645					650					655		
tta	caa	act	ata	tca	aat	gcc	caa	gct	agt	ata	tat	aaa	ttt	gat	agt	2016
Leu	Gln	Thr	Ile	Ser	Asn	Ala	Gln	Ala	Ser	Ile	Tyr	Lys	Phe	Asp	Ser	
			660					665					670			
ttg	aac	atg	tct	ata	tta	aat	gat	aat	tat	gaa	aat	gaa	ata	aaa	aat	2064
Leu	Asn	Met	Ser	Ile	Leu	Asn	Asp	Asn	Tyr	Glu	Asn	Glu	Ile	Lys	Asn	
		675					680					685				
aaa	ttt	atg	aca	cat	cac	aaa	ata	caa	tat	ttt	gga	gtt	ata	gag	tg	2112
Lys	Phe	Met	Thr	His	His	Lys	Ile	Gln	Tyr	Phe	Gly	Val	Ile	Glu	Trp	
	690					695					700					
caa	tta	gct	att	cat	tat	tct	tac	aat	aac	aat	aca	aaa	gat	atg	ata	2160
Gln	Leu	Ala	Ile	His	Tyr	Ser	Tyr	Asn	Asn	Asn	Thr	Lys	Asp	Met	Ile	
705					710					715				720		
tta	tta	aaa	cta	aaa	aat	tta	tca	aac	gat	gga	aca	aaa	gta	ata	ata	2208
Leu	Leu	Lys	Leu	Lys	Asn	Leu	Ser	Asn	Asp	Gly	Thr	Lys	Val	Ile	Ile	
				725					730					735		
act	tgt	ctt	gac	gga	gac	gaa	ata	aca	aat	aga	tta	aat	gaa	aat	cct	2256
Thr	Cys	Leu	Asp	Gly	Asp	Glu	Ile	Thr	Asn	Arg	Leu	Asn	Glu	Asn	Pro	
			740					745					750			
aat	tta	att	tat	aat	att	caa	ccc	gga	att	aca	tat	aaa	att	tct	aaa	2304
Asn	Leu	Ile	Tyr	Asn	Ile	Gln	Pro	Gly	Ile	Thr	Tyr	Lys	Ile	Ser	Lys	

755	760	765	
att tca gat gat aaa ata tca gtt tta tat aat gct aca atg act gaa			2352
Ile Ser Asp Asp Lys Ile Ser Val Leu Tyr Asn Ala Thr Met Thr Glu			
770	775	780	
tggtta gaa gaa tat ata ata aca gat aaa ata att gat gat ttt gct			2400
Trp Leu Glu Glu Tyr Ile Ile Thr Asp Lys Ile Ile Asp Asp Phe Ala			
785	790	795	800
atg tat aat ttt ata tta tca gat gtt tgt aaa ttt gat gat ata ttt			2448
Met Tyr Asn Phe Ile Leu Ser Asp Val Cys Lys Phe Asp Asp Ile Phe			
	805	810	815
aaa tat aat tct gat aaa tct gta gaa gtt tta tct aat ttt tta aga			2496
Lys Tyr Asn Ser Asp Lys Ser Val Glu Val Leu Ser Asn Phe Leu Arg			
	820	825	830
aaa tca act aaa aag ttt tat aat gat att aaa aat gat aaa aat ata			2544
Lys Ser Thr Lys Lys Phe Tyr Asn Asp Ile Lys Asn Asp Lys Asn Ile			
	835	840	845
tat aac aat gat gat att aaa aaa ata atg tcg tta ttt aaa gtt tat			2592
Tyr Asn Asn Asp Asp Ile Lys Lys Ile Met Ser Leu Phe Lys Val Tyr			
	850	855	860
act ttt gtt tat tca tct tgt aaa taa			2619
Thr Phe Val Tyr Ser Ser Cys Lys			
865	870		

&lt;210&gt; 47

&lt;211&gt; 3450

&lt;212&gt; DNA

&lt;213&gt; Amsacta moorei entomopoxvirus

&lt;220&gt;

&lt;221&gt; exon

&lt;222&gt; (1) .. (3450)

&lt;223&gt;

&lt;400&gt; 47

atg aga aat aat aaa gaa aag tat atg aat cat ttt acg gat ttt ata	48
Met Arg Asn Asn Lys Glu Lys Tyr Met Asn His Phe Thr Asp Phe Ile	
1 5 10 15	
att cgt aat tta cca ttt aga aat tta att gat tcg atg aaa gaa aat	96

Ile	Arg	Asn	Leu	Pro	Phe	Arg	Asn	Leu	Ile	Asp	Ser	Met	Lys	Glu	Asn		
		20						25					30				
att	att	att	aat	aat	gaa	aca	tat	aaa	ata	gaa	gaa	tta	ttt	aaa	tat	144	
Ile	Ile	Ile	Asn	Asn	Glu	Thr	Tyr	Lys	Ile	Glu	Glu	Leu	Phe	Lys	Tyr		
		35					40					45					
att	tat	tat	cat	cca	cta	gat	tta	tta	aca	att	aga	gac	att	agt	aat	192	
Ile	Tyr	Tyr	His	Pro	Leu	Asp	Leu	Leu	Thr	Ile	Arg	Asp	Ile	Ser	Asn		
	50					55					60						
gca	gat	aga	aaa	gat	gaa	tat	gtt	aaa	caa	ttt	gta	aat	aat	tta	tat	240	
Ala	Asp	Arg	Lys	Asp	Glu	Tyr	Val	Lys	Gln	Phe	Val	Asn	Asn	Leu	Tyr		
65					70				75					80			
ctt	aga	tat	gca	tat	aac	gaa	atg	gat	ttt	ata	aaa	aat	aat	ata	aga	288	
Leu	Arg	Tyr	Ala	Tyr	Asn	Glu	Met	Asp	Phe	Ile	Lys	Asn	Asn	Ile	Arg		
			85						90					95			
tat	gac	gat	aaa	gta	tat	tct	att	ata	aac	gaa	att	aat	tat	ttt	cca	336	
Tyr	Asp	Asp	Lys	Val	Tyr	Ser	Ile	Ile	Asn	Glu	Ile	Asn	Tyr	Phe	Pro		
			100					105					110				
gaa	cat	act	tcg	gaa	ttt	tta	aaa	tat	aga	tta	tca	cac	tat	gaa	tca	384	
Glu	His	Thr	Ser	Glu	Phe	Leu	Lys	Tyr	Arg	Leu	Ser	His	Tyr	Glu	Ser		
		115					120					125					
gaa	tca	aga	atc	aga	gga	gga	aga	gta	gta	act	ttt	agc	ggg	gtt	cct	432	
Glu	Ser	Arg	Ile	Arg	Gly	Gly	Arg	Val	Val	Thr	Phe	Ser	Gly	Val	Pro		
	130					135					140						
gat	aat	ggg	tat	ggg	tat	tta	tta	agt	caa	tca	gac	cct	tca	tct	aag	480	
Asp	Asn	Gly	Tyr	Gly	Tyr	Leu	Leu	Ser	Gln	Ser	Asp	Pro	Ser	Ser	Lys		
145					150				155						160		
tat	ata	tgg	gca	ata	gta	gat	aac	tat	tta	atg	att	gat	aat	gaa	gat	528	
Tyr	Ile	Trp	Ala	Ile	Val	Asp	Asn	Tyr	Leu	Met	Ile	Asp	Asn	Glu	Asp		
			165						170					175			
aaa	ttt	gat	ttt	tat	acc	caa	tat	att	cca	ttt	att	aat	tat	ttt	cta	576	
Lys	Phe	Asp	Phe	Tyr	Thr	Gln	Tyr	Ile	Pro	Phe	Ile	Asn	Tyr	Phe	Leu		
			180					185					190				
aaa	tta	tat	tat	aat	aac	atc	aca	aaa	aaa	tat	att	att	tta	gat	cct	624	
Lys	Leu	Tyr	Tyr	Asn	Asn	Ile	Thr	Lys	Lys	Tyr	Ile	Ile	Leu	Asp	Pro		
		195					200					205					
agt	aat	cct	gaa	gaa	aat	aaa	gat	gta	cct	aac	gct	aat	tta	atc	gac	672	
Ser	Asn	Pro	Glu	Glu	Asn	Lys	Asp	Val	Pro	Asn	Ala	Asn	Leu	Ile	Asp		
	210					215					220						
gaa	agt	tta	aaa	aat	aaa	tat	aat	aat	ttt	aca	aag	aaa	tta	tca	tat	720	
Glu	Ser	Leu	Lys	Asn	Lys	Tyr	Asn	Asn	Phe	Thr	Lys	Lys	Leu	Ser	Tyr		
225					230				235						240		
ttt	gat	ata	tca	aat	agt	aga	tat	aat	tct	ata	aat	gat	gtg	ggg	gat	768	
Phe	Asp	Ile	Ser	Asn	Ser	Arg	Tyr	Asn	Ser	Ile	Asn	Asp	Val	Gly	Asp		

245	250	255	
ttt aat aat tat tta gat atc aat act aat aaa aat att att gaa aat Phe Asn Asn Tyr Leu Asp Ile Asn Thr Asn Lys Asn Ile Ile Glu Asn 260 265 270			816
tat gat gta att att aat aat att ata aaa tca ata tat cta tat aac Tyr Asp Val Ile Ile Asn Asn Ile Ile Lys Ser Ile Tyr Leu Tyr Asn 275 280 285			864
ata atg gat aca aat gta gaa gat ata tta aat ata ata atg aac gat Ile Met Asp Thr Asn Val Glu Asp Ile Leu Asn Ile Ile Met Asn Asp 290 295 300			912
aca aat tat tta tta ttg aat gaa ata tat agt gaa tat tta cca aac Thr Asn Tyr Leu Leu Leu Asn Glu Ile Tyr Ser Glu Tyr Leu Pro Asn 305 310 315 320			960
tca agc aaa tta tat gtt tta gtg gga tta cgt cgc att ata tat gaa Ser Ser Lys Leu Tyr Val Leu Val Gly Leu Arg Arg Ile Ile Tyr Glu 325 330 335			1008
aaa agc aaa caa aat aaa aat att agc aat tta tat atg tta gat tca Lys Ser Lys Gln Asn Lys Asn Ile Ser Asn Leu Tyr Met Leu Asp Ser 340 345 350			1056
ttt gta agt ata tta tta tat tta tta gaa aga tat tac gaa aat gat Phe Val Ser Ile Leu Leu Tyr Leu Leu Glu Arg Tyr Tyr Glu Asn Asp 355 360 365			1104
ata acc aca ctt aat gaa tct aaa aga tta ata aaa caa tat tat aaa Ile Thr Thr Leu Asn Glu Ser Lys Arg Leu Ile Lys Gln Tyr Tyr Lys 370 375 380			1152
gat aat tta aat tca aaa aat agc gtt aat ttg gat tct ata aat att Asp Asn Leu Asn Ser Lys Asn Ser Val Asn Leu Asp Ser Ile Asn Ile 385 390 395 400			1200
att aaa gaa aat atc aat aat aat att att aat ata aca tta gat gaa Ile Lys Glu Asn Ile Asn Asn Asn Ile Ile Asn Ile Thr Leu Asp Glu 405 410 415			1248
gat gaa caa tca aga tat aat tta ata ata gcc aca aac cca gaa ata Asp Glu Gln Ser Arg Tyr Asn Leu Ile Ile Ala Thr Asn Pro Glu Ile 420 425 430			1296
ata gta aat tat gca agt aga aat tat ttt aac atc agt agt aac gaa Ile Val Asn Tyr Ala Ser Arg Asn Tyr Phe Asn Ile Ser Ser Asn Glu 435 440 445			1344
gat aac aca tca aat gtg tat aaa aaa gca atg gca ttt ttc ata aat Asp Asn Thr Ser Asn Val Tyr Lys Lys Ala Met Ala Phe Phe Ile Asn 450 455 460			1392
aat ttt att gaa aat aat ata act aac gaa aat ata ata aat aat tta Asn Phe Ile Glu Asn Asn Ile Thr Asn Glu Asn Ile Ile Asn Asn Leu 465 470 475 480			1440

tca caa gtt tat act caa aat aca gat ttt att aat att act tat gat	1488
Ser Gln Val Tyr Thr Gln Asn Thr Asp Phe Ile Asn Ile Thr Tyr Asp	
485 490 495	
gat cta aat aat tta aaa ata aaa tat att aat aat tat aat ata aat	1536
Asp Leu Asn Asn Leu Lys Ile Lys Tyr Ile Asn Asn Tyr Asn Ile Asn	
500 505 510	
tta gat att aaa aaa att att aat gac aat cta gaa ata att aga att	1584
Leu Asp Ile Lys Lys Ile Ile Asn Asp Asn Leu Glu Ile Ile Arg Ile	
515 520 525	
tat aaa gat aat gtt tta tat gac act aat att aaa atg aat tat aaa	1632
Tyr Lys Asp Asn Val Leu Tyr Asp Thr Asn Ile Lys Met Asn Tyr Lys	
530 535 540	
tca ttt ata tca cta tta ccc acc ata tac tat att att ttt tat aat	1680
Ser Phe Ile Ser Leu Leu Pro Thr Ile Tyr Tyr Ile Ile Phe Tyr Asn	
545 550 555 560	
caa cct ata aat aga aaa ata tat aga aaa gct ata att caa gaa cct	1728
Gln Pro Ile Asn Arg Lys Ile Tyr Arg Lys Ala Ile Ile Gln Glu Pro	
565 570 575	
cca att gaa gaa gag atc tca act gaa act aca aaa aga gct aga aga	1776
Pro Ile Glu Glu Glu Ile Ser Thr Glu Thr Thr Lys Arg Ala Arg Arg	
580 585 590	
gtg aga ttt aat cca ttt aat gtc gaa gaa aca ata ata gaa ccc aag	1824
Val Arg Phe Asn Pro Phe Asn Val Glu Glu Thr Ile Ile Glu Pro Lys	
595 600 605	
agt gtt ttt gtt aat aaa agt aaa aat tat tta tat gat aca tta ttt	1872
Ser Val Phe Val Asn Lys Ser Lys Asn Tyr Leu Tyr Asp Thr Leu Phe	
610 615 620	
tgg tct ggc ata tct ata gat gat ttt aat aaa ttt cca tta tac att	1920
Trp Ser Gly Ile Ser Ile Asp Asp Phe Asn Lys Phe Pro Leu Tyr Ile	
625 630 635 640	
aaa act att atc ttg gat agt tgt ctt att tta gga aga caa ata aac	1968
Lys Thr Ile Ile Leu Asp Ser Cys Leu Ile Leu Gly Arg Gln Ile Asn	
645 650 655	
gat gat ggg tca tct act tgc gtt tta tat cat gat att aat aat aac	2016
Asp Asp Gly Ser Ser Thr Cys Val Leu Tyr His Asp Ile Asn Asn Asn	
660 665 670	
gat gtt aca aaa ata tgt ata ata cct tat cct tat aca gca aac aga	2064
Asp Val Thr Lys Ile Cys Ile Ile Pro Tyr Pro Tyr Thr Ala Asn Arg	
675 680 685	
act atg tat gat gtt ttt aaa caa gtt tca gat aaa tta aga tct atg	2112
Thr Met Tyr Asp Val Phe Lys Gln Val Ser Asp Lys Leu Arg Ser Met	
690 695 700	

tac tca tat cct gta aat tat aat ata aat aat aat gaa aaa cat tta	2160
Tyr Ser Tyr Pro Val Asn Tyr Asn Ile Asn Asn Asn Glu Lys His Leu	
705 710 715 720	
aat tta tca aaa aaa gga aat tat aaa ttt atg aat aaa cta gca gaa	2208
Asn Leu Ser Lys Lys Gly Asn Tyr Lys Phe Met Asn Lys Leu Ala Glu	
725 730 735	
tgt aaa gat att aaa gat tta ata caa ttt tat gtt atg gta aga gat	2256
Cys Lys Asp Ile Lys Asp Leu Ile Gln Phe Tyr Val Met Val Arg Asp	
740 745 750	
aca gat cca ggt cat tct gaa ata tca ata cca cca aac caa gaa tta	2304
Thr Asp Pro Gly His Ser Glu Ile Ser Ile Pro Pro Asn Gln Glu Leu	
755 760 765	
tat tta gca ata act tta tta gat tta ttg gga ttt tct cct act tta	2352
Tyr Leu Ala Ile Thr Leu Leu Asp Leu Leu Gly Phe Ser Pro Thr Leu	
770 775 780	
tca aga aga aat act agt att ggt ttt tca tat tac att caa aca gat	2400
Ser Arg Arg Asn Thr Ser Ile Gly Phe Ser Tyr Tyr Ile Gln Thr Asp	
785 790 795 800	
aga caa gta tct gct cgt aat ttg ata tat ata tta tca aga aac tac	2448
Arg Gln Val Ser Ala Arg Asn Leu Ile Tyr Ile Leu Ser Arg Asn Tyr	
805 810 815	
cca gat atg gta aaa agt aag gaa tta tca gat gta gta att aat ata	2496
Pro Asp Met Val Lys Ser Lys Glu Leu Ser Asp Val Val Ile Asn Ile	
820 825 830	
ttg tcg cca ata ctt gca tat tta aga tat gta tta aat tat tat aga	2544
Leu Ser Pro Ile Leu Ala Tyr Leu Arg Tyr Val Leu Asn Tyr Tyr Arg	
835 840 845	
aca aat aat aca aca tta aca gct gga tct aat aat gca ggt cat gat	2592
Thr Asn Asn Thr Thr Leu Thr Ala Gly Ser Asn Asn Ala Gly His Asp	
850 855 860	
tgt tgt att cct att aaa tca aat cct tta gat tta ctt att aat ata	2640
Cys Cys Ile Pro Ile Lys Ser Asn Pro Leu Asp Leu Leu Ile Asn Ile	
865 870 875 880	
gat aca tct ttt act gat tcc gac aat ata tta gat ata atg aat aga	2688
Asp Thr Ser Phe Thr Asp Ser Asp Asn Ile Leu Asp Ile Met Asn Arg	
885 890 895	
gat atg ttt aat ttg gat aat gat ata ttt aga caa gta ata caa aat	2736
Asp Met Phe Asn Leu Asp Asn Asp Ile Phe Arg Gln Val Ile Gln Asn	
900 905 910	
aat att tat agc gct ggt agc gtt gat att gtc gat att ata act gat	2784
Asn Ile Tyr Ser Ala Gly Ser Val Asp Ile Val Asp Ile Ile Thr Asp	
915 920 925	
aat att ccc caa aac att tat atg aaa aca aac ata att gat aaa atg	2832



Asn Ile Pro Gln Asn Ile Tyr Met Lys Thr Asn Ile Ile Asp Lys Met	
930 935 940	
tat gat aaa att ttt gct ggt gaa agt att agc gat ata ttg gat ata	2880
Tyr Asp Lys Ile Phe Ala Gly Glu Ser Ile Ser Asp Ile Leu Asp Ile	
945 950 955 960	
cag ttt gat gaa gat att aat gat aat ttt aat tac aat gat gta aat	2928
Gln Phe Asp Glu Asp Ile Asn Asp Asn Phe Asn Tyr Asn Asp Val Asn	
965 970 975	
atg att act aat gat tta atg aaa aaa cta aga aaa tta tta aaa aaa	2976
Met Ile Thr Asn Asp Leu Met Lys Lys Leu Arg Lys Leu Leu Lys Lys	
980 985 990	
aca act att aat aat tta gaa gac aat gct atg ata tta aag tca caa	3024
Thr Thr Ile Asn Asn Leu Glu Asp Asn Ala Met Ile Leu Lys Ser Gln	
995 1000 1005	
atg tta tca tct att aat aat gtt ttt aat cgt tat tct tgt atg	3069
Met Leu Ser Ser Ile Asn Asn Val Phe Asn Arg Tyr Ser Cys Met	
1010 1015 1020	
gaa aaa ata cca aca caa tat ctt ata aat att aga aca tta tta	3114
Glu Lys Ile Pro Thr Gln Tyr Leu Ile Asn Ile Arg Thr Leu Leu	
1025 1030 1035	
aaa caa tat agt aat gaa aat ata aaa att gac gaa gat tta aaa	3159
Lys Gln Tyr Ser Asn Glu Asn Ile Lys Ile Asp Glu Asp Leu Lys	
1040 1045 1050	
aat aat atc caa aca ata att agt aat atc cat agt aat act aaa	3204
Asn Asn Ile Gln Thr Ile Ile Ser Asn Ile His Ser Asn Thr Lys	
1055 1060 1065	
gat ata att aaa att att acc act tta agt gct ggt att gat tta	3249
Asp Ile Ile Lys Ile Ile Thr Thr Leu Ser Ala Gly Ile Asp Leu	
1070 1075 1080	
gtt aga gca tta aaa aga tct aat gca aat gta gaa aat aaa aca	3294
Val Arg Ala Leu Lys Arg Ser Asn Ala Asn Val Glu Asn Lys Thr	
1085 1090 1095	
ata aat ctt gaa ttt cta aaa aaa tta tgt gat att tgt aaa gat	3339
Ile Asn Leu Glu Phe Leu Lys Lys Leu Cys Asp Ile Cys Lys Asp	
1100 1105 1110	
agt ttt tat aaa tat aat aga aat aat gat ata gta tat aaa aat	3384
Ser Phe Tyr Lys Tyr Asn Arg Asn Asn Asp Ile Val Tyr Lys Asn	
1115 1120 1125	
tta cta aaa gat gta ttt aat aat gat aat gaa att aat aat gat	3429
Leu Leu Lys Asp Val Phe Asn Asn Asp Asn Glu Ile Asn Asn Asp	
1130 1135 1140	
agt gtg ttt gat aca tgt taa	3450
Ser Val Phe Asp Thr Cys	

1145

&lt;210&gt; 48

&lt;211&gt; 2007

&lt;212&gt; DNA

&lt;213&gt; Amsacta moorei entomopoxvirus

&lt;220&gt;

&lt;221&gt; exon

&lt;222&gt; (1) .. (2007)

&lt;223&gt;

&lt;400&gt; 48

atg aat gtt ttt gaa atg gat agt ata aat ata tct aat cgt aat tat	48
Met Asn Val Phe Glu Met Asp Ser Ile Asn Ile Ser Asn Arg Asn Tyr	
1 5 10 15	
tta ata gca ggt gta aca tct gat aat att tgt aat tgt gtt aat gat	96
Leu Ile Ala Gly Val Thr Ser Asp Asn Ile Cys Asn Cys Val Asn Asp	
20 25 30	
agt gct atg gat gat tat tta ttt gat aca tta tct gta gat aga tta	144
Ser Ala Met Asp Asp Tyr Leu Phe Asp Thr Leu Ser Val Asp Arg Leu	
35 40 45	
gat ggc gga tat ata aaa cac gaa tgt ggt ata gaa tgt ggg tgt ttt	192
Asp Gly Gly Tyr Ile Lys His Glu Cys Gly Ile Glu Cys Gly Cys Phe	
50 55 60	
aat ggt aaa tta atg gct agt atg gcg aca gaa atg tca aga gat aat	240
Asn Gly Lys Leu Met Ala Ser Met Ala Thr Glu Met Ser Arg Asp Asn	
65 70 75 80	
tta ata gca tcg tgt tct aaa agt gca gga gct tct aat gta aaa tca	288
Leu Ile Ala Ser Cys Ser Lys Ser Ala Gly Ala Ser Asn Val Lys Ser	
85 90 95	
tct aat aat caa aat caa aaa aaa aga aaa tca gaa tct ggt aat aaa	336
Ser Asn Asn Gln Asn Gln Lys Lys Arg Lys Ser Glu Ser Gly Asn Lys	
100 105 110	
att caa aaa caa tta gat att atg aac aca aaa gaa gat cat att aag	384
Ile Gln Lys Gln Leu Asp Ile Met Asn Thr Lys Glu Asp His Ile Lys	
115 120 125	
aaa att gct gaa tat gta gct aat aat tta cca aaa tca cct tta aca	432

Lys	Ile	Ala	Glu	Tyr	Val	Ala	Asn	Asn	Leu	Pro	Lys	Ser	Pro	Leu	Thr		
130						135					140						
tat	aca	gtt	cac	gac	att	aat	aga	tta	att	atc	aca	tct	cct	ttt	aag	480	
Tyr	Thr	Val	His	Asp	Ile	Asn	Arg	Leu	Ile	Ile	Thr	Ser	Pro	Phe	Lys		
145					150				155						160		
gat	gtt	att	tta	aac	gaa	aat	gat	atg	aaa	tct	ata	atc	gga	ttg	gct	528	
Asp	Val	Ile	Leu	Asn	Glu	Asn	Asp	Met	Lys	Ser	Ile	Ile	Gly	Leu	Ala		
				165					170					175			
gca	gct	ttt	tat	aaa	aat	aaa	aca	ata	aat	cat	tca	tta	tta	tca	act	576	
Ala	Ala	Phe	Tyr	Lys	Asn	Lys	Thr	Ile	Asn	His	Ser	Leu	Leu	Ser	Thr		
			180					185					190				
att	aat	att	aat	aca	aat	gat	ctt	att	caa	caa	tta	aga	caa	gta	tat	624	
Ile	Asn	Ile	Asn	Thr	Asn	Asp	Leu	Ile	Gln	Gln	Leu	Arg	Gln	Val	Tyr		
	195						200					205					
aat	tta	tca	aca	tta	gta	gat	tat	gat	tca	ttt	tta	aat	aat	tta	aaa	672	
Asn	Leu	Ser	Thr	Leu	Val	Asp	Tyr	Asp	Ser	Phe	Leu	Asn	Asn	Leu	Lys		
	210					215					220						
gta	gcc	agt	gtg	gaa	tat	act	gat	att	gca	gat	tgt	aat	gat	tac	att	720	
Val	Ala	Ser	Val	Glu	Tyr	Thr	Asp	Ile	Ala	Asp	Cys	Asn	Asp	Tyr	Ile		
225					230				235						240		
aaa	tat	gtg	cca	gac	gaa	cct	aat	gtt	cca	tca	ata	tta	ttt	gct	tta	768	
Lys	Tyr	Val	Pro	Asp	Glu	Pro	Asn	Val	Pro	Ser	Ile	Leu	Phe	Ala	Leu		
				245					250					255			
ttt	tct	aca	aga	ata	cct	gta	tta	ttt	gat	att	gtt	gta	aat	caa	gat	816	
Phe	Ser	Thr	Arg	Ile	Pro	Val	Leu	Phe	Asp	Ile	Val	Val	Asn	Gln	Asp		
			260					265					270				
tta	ttt	aaa	tta	caa	caa	gag	tta	cag	aca	gat	gat	tat	agc	gca	tat	864	
Leu	Phe	Lys	Leu	Gln	Gln	Glu	Leu	Gln	Thr	Asp	Asp	Tyr	Ser	Ala	Tyr		
		275					280					285					
aaa	aat	ata	tat	cta	ttg	ctt	ttt	aga	tta	tct	gat	aga	gaa	cca	tac	912	
Lys	Asn	Ile	Tyr	Leu	Leu	Leu	Phe	Arg	Leu	Ser	Asp	Arg	Glu	Pro	Tyr		
	290					295					300						
tat	tca	aat	caa	tct	gga	gga	ctt	agt	aat	aaa	att	gat	gtt	tat	act	960	
Tyr	Ser	Asn	Gln	Ser	Gly	Gly	Leu	Ser	Asn	Lys	Ile	Asp	Val	Tyr	Thr		
305					310				315						320		
gaa	tta	agt	cgt	ata	tta	tta	tct	atg	tcg	att	aaa	aga	tta	ata	tta	1008	
Glu	Leu	Ser	Arg	Ile	Leu	Leu	Ser	Met	Ser	Ile	Lys	Arg	Leu	Ile	Leu		
				325					330					335			
aaa	att	att	aaa	ggc	aca	gtt	aca	gga	aac	aca	gta	gct	cct	ata	atg	1056	
Lys	Ile	Ile	Lys	Gly	Thr	Val	Thr	Gly	Asn	Thr	Val	Ala	Pro	Ile	Met		
			340					345					350				
aat	ata	ttt	aaa	aat	tta	tat	att	aaa	aat	gtc	aga	tct	tct	caa	gaa	1104	
Asn	Ile	Phe	Lys	Asn	Leu	Tyr	Ile	Lys	Asn	Val	Arg	Ser	Ser	Gln	Glu		

355	360	365	
gct tta tta tca gca att tta aaa ata tgg tca tat gct cca aca att			1152
Ala Leu Leu Ser Ala Ile Leu Lys Ile Trp Ser Tyr Ala Pro Thr Ile			
370	375	380	
ggt ctg aaa aat ata tca tct gat ttt aga aca gaa act gta ttt ttt			1200
Val Leu Lys Asn Ile Ser Ser Asp Phe Arg Thr Glu Thr Val Phe Phe			
385	390	395	400
ggt gaa tat gaa ata tct gaa tac aat caa ttt gaa aat caa aat ata			1248
Val Glu Tyr Glu Ile Ser Glu Tyr Asn Gln Phe Glu Asn Gln Asn Ile			
	405	410	415
aaa ttc act caa gaa tta atg aaa tat att tat tac gat cct att gtt			1296
Lys Phe Thr Gln Glu Leu Met Lys Tyr Ile Tyr Tyr Asp Pro Ile Val			
	420	425	430
aat aaa gtt att ttg tct cct aaa tat att ttg gat tcg ata ggc gga			1344
Asn Lys Val Ile Leu Ser Pro Lys Tyr Ile Leu Asp Ser Ile Gly Gly			
	435	440	445
aac aca ggt atg caa agt ata aca tat tgt aat agt ggt ttt aga agt			1392
Asn Thr Gly Met Gln Ser Ile Thr Tyr Cys Asn Ser Gly Phe Arg Ser			
	450	455	460
att aat cct atg aca aat gta gct tta aaa tca aca ggt atg ttc att			1440
Ile Asn Pro Met Thr Asn Val Ala Leu Lys Ser Thr Gly Met Phe Ile			
465	470	475	480
tta tct ata cct aga tta att aaa caa tca tat tct tat ggt tta cct			1488
Leu Ser Ile Pro Arg Leu Ile Lys Gln Ser Tyr Ser Tyr Gly Leu Pro			
	485	490	495
gac gaa ttt tct gat aga tta tta act aaa tat gta gat tta gat caa			1536
Asp Glu Phe Ser Asp Arg Leu Leu Thr Lys Tyr Val Asp Leu Asp Gln			
	500	505	510
aat att acc att ggt tgt aat atg ttt caa tta aga gcg gcc gtt tgt			1584
Asn Ile Thr Ile Gly Cys Asn Met Phe Gln Leu Arg Ala Ala Val Cys			
	515	520	525
tac aaa ata tca aaa tat gtt gat tta gat aca tgt ata cag aat cct			1632
Tyr Lys Ile Ser Lys Tyr Val Asp Leu Asp Thr Cys Ile Gln Asn Pro			
	530	535	540
ata tca tta gga aca gtt gct att gta aaa aca caa aaa ggg tgg att			1680
Ile Ser Leu Gly Thr Val Ala Ile Val Lys Thr Gln Lys Gly Trp Ile			
545	550	555	560
aga tat aat cca gat tta atg tat tct tgt aac gaa aag aaa gat tta			1728
Arg Tyr Asn Pro Asp Leu Met Tyr Ser Cys Asn Glu Lys Lys Asp Leu			
	565	570	575
tta gat aaa ata cta aga aat gaa tat aaa aaa tca ttg aat tta aat			1776
Leu Asp Lys Ile Leu Arg Asn Glu Tyr Lys Lys Ser Leu Asn Leu Asn			
	580	585	590

aat tat gaa gtt aat caa tat tta gat aaa gat tac gaa gaa tgg aaa 1824  
 Asn Tyr Glu Val Asn Gln Tyr Leu Asp Lys Asp Tyr Glu Glu Trp Lys  
           595                                600                                605

agt act ttt tca tct att aat aat att atc gat aaa ttt gaa aaa ggt 1872  
 Ser Thr Phe Ser Ser Ile Asn Asn Ile Ile Asp Lys Phe Glu Lys Gly  
           610                                615                                620

tac gta agt aca gat tca tta att att caa gag gca gaa gcc atc gat 1920  
 Tyr Val Ser Thr Asp Ser Leu Ile Ile Gln Glu Ala Glu Ala Ile Asp  
           625                                630                                635                                640

ata att agt aga tat gga act att ata ata tac gca caa gaa tat act 1968  
 Ile Ile Ser Arg Tyr Gly Thr Ile Ile Ile Tyr Ala Gln Glu Tyr Thr  
                                 645                                650                                655

aat ggt gta gat atg tta cca ctg aga aga tat tat taa 2007  
 Asn Gly Val Asp Met Leu Pro Leu Arg Arg Tyr Tyr  
                                 660                                665

<210> 49

<211> 723

<212> DNA

<213> Amsacta moorei entomopoxvirus

<220>

<221> exon

<222> (1) .. (723)

<223>

<400> 49  
 atg tcc gaa ttc gat tat gat aaa ctg cgt gct aaa cca ttt aat atg 48  
 Met Ser Glu Phe Asp Tyr Asp Lys Leu Arg Ala Lys Pro Phe Asn Met  
   1                                5                                10                                15

gca att ata gga aaa aca gga tca ggt aaa act aca ttt tta aag aat 96  
 Ala Ile Ile Gly Lys Thr Gly Ser Gly Lys Thr Thr Phe Leu Lys Asn  
           20                                25                                30

tta tta tta aaa att ggt tac gga ttt tat aaa ttt ata tat tta att 144  
 Leu Leu Leu Lys Ile Gly Tyr Gly Phe Tyr Lys Phe Ile Tyr Leu Ile  
           35                                40                                45

act agt tct gaa gtt aac ttt aaa tca aat gaa tat ttt aaa ttt att 192  
 Thr Ser Ser Glu Val Asn Phe Lys Ser Asn Glu Tyr Phe Lys Phe Ile

50	55	60	
tat ccc aat cat gtt ttt tat ctt tat tcg aat aac aaa gac aag gat			240
Tyr Pro Asn His Val Phe Tyr Leu Tyr Ser Asn Asn Lys Asp Lys Asp			
65	70	75	80
gtt aaa tat tta tta caa gca tat tta gaa aaa att aaa aat ttt agt			288
Val Lys Tyr Leu Leu Gln Ala Tyr Leu Glu Lys Ile Lys Asn Phe Ser			
	85	90	95
ttt gaa atg aat caa aag tgt gaa aat ttt aga aca tta gtt att tat			336
Phe Glu Met Asn Gln Lys Cys Glu Asn Phe Arg Thr Leu Val Ile Tyr			
	100	105	110
gat gat att ggc aaa gac aca aaa gat aaa tta agt aat ttt aca aat			384
Asp Asp Ile Gly Lys Asp Thr Lys Asp Lys Leu Ser Asn Phe Thr Asn			
	115	120	125
gtg tgc aga cat tcg tta gta tca aat att ttt cta gtt cat aga tta			432
Val Cys Arg His Ser Leu Val Ser Asn Ile Phe Leu Val His Arg Leu			
	130	135	140
gaa cat tta gat aca act aca aga gat agt tta tca tat cat gtt ata			480
Glu His Leu Asp Thr Thr Thr Arg Asp Ser Leu Ser Tyr His Val Ile			
	145	150	155
aat tcc gaa tca gaa aat atg gat tta ata cct tgt aat aaa aat cta			528
Asn Ser Glu Ser Glu Asn Met Asp Leu Ile Pro Cys Asn Lys Asn Leu			
	165	170	175
aga aat tca tta ctt gca tct gtg ata aat att ttt aaa gat cgc gaa			576
Arg Asn Ser Leu Leu Ala Ser Val Ile Asn Ile Phe Lys Asp Arg Glu			
	180	185	190
caa tca aaa tat tat ata tat tgt ata ata tat gat tct gta tct tat			624
Gln Ser Lys Tyr Tyr Ile Tyr Cys Ile Ile Tyr Asp Ser Val Ser Tyr			
	195	200	205
tct tgt tta ata tca gac gat gat tta gaa aat ata aaa aat gaa gat			672
Ser Cys Leu Ile Ser Asp Asp Asp Leu Glu Asn Ile Lys Asn Glu Asp			
	210	215	220
aaa tat gta ttt tat act gat tcc gtg att aaa tct cat ata cta aat			720
Lys Tyr Val Phe Tyr Thr Asp Ser Val Ile Lys Ser His Ile Leu Asn			
	225	230	235
taa			723

&lt;210&gt; 50

&lt;211&gt; 1407

&lt;212&gt; DNA

&lt;213&gt; Amsacta moorei entomopoxvirus

&lt;220&gt;

&lt;221&gt; exon

&lt;222&gt; (1) .. (1407)

&lt;223&gt;

&lt;400&gt; 50

atg agt aat att gaa ata tat gat atg ttt gaa ggt gat aag gaa gta	48
Met Ser Asn Ile Glu Ile Tyr Asp Met Phe Glu Gly Asp Lys Glu Val	
1 5 10 15	
cta ttt ata gct ggt tca cat ata aat gaa tta aaa gct gat aaa aat	96
Leu Phe Ile Ala Gly Ser His Ile Asn Glu Leu Lys Ala Asp Lys Asn	
20 25 30	
tta tgt agt gaa gtt ata aat aat gtt gtt aat gat ttt tcg ttt tct	144
Leu Cys Ser Glu Val Ile Asn Asn Val Val Asn Asp Phe Ser Phe Ser	
35 40 45	
aac att gaa aaa aac ttt aaa aat ata aaa aaa att aat aaa ttt aaa	192
Asn Ile Glu Lys Asn Phe Lys Asn Ile Lys Lys Ile Asn Lys Phe Lys	
50 55 60	
tat aaa att att aat gat att aca aat gta act gaa aca gat tat ttt	240
Tyr Lys Ile Ile Asn Asp Ile Thr Asn Val Thr Glu Thr Asp Tyr Phe	
65 70 75 80	
aaa cca tat ttt aaa atg aaa cca tat atg gct aat caa tat ata tat	288
Lys Pro Tyr Phe Lys Met Lys Pro Tyr Met Ala Asn Gln Tyr Ile Tyr	
85 90 95	
cat ata cat act gga gga tat ggc atg act gtt cgt att aat gaa agt	336
His Ile His Thr Gly Gly Tyr Gly Met Thr Val Arg Ile Asn Glu Ser	
100 105 110	
ttt tgt ttt aaa ata tca tta aat cca act aat aat cag ata cat gaa	384
Phe Cys Phe Lys Ile Ser Leu Asn Pro Thr Asn Asn Gln Ile His Glu	
115 120 125	
ttt gta ata ccc agg atg tta tct agt att ata tct tat tca aac gca	432
Phe Val Ile Pro Arg Met Leu Ser Ser Ile Ile Ser Tyr Ser Asn Ala	
130 135 140	
gac aaa tta ata tta tta cca tat aca tta ata aag aat ata aat ttc	480
Asp Lys Leu Ile Leu Leu Pro Tyr Thr Leu Ile Lys Asn Ile Asn Phe	
145 150 155 160	
aat gga ttg ata tat ata ata agt atg cat aat ata att tta tta tta	528
Asn Gly Leu Ile Tyr Ile Ile Ser Met His Asn Ile Ile Leu Leu Leu	
165 170 175	

att aat ttt ata tta gat aaa aat tat agt aat att gat ata tat aat Ile Asn Phe Ile Leu Asp Lys Asn Tyr Ser Asn Ile Asp Ile Tyr Asn 180 185 190	576
aca tat tta gat ttt aat aaa atg aat agt att tat aga tct tta aca Thr Tyr Leu Asp Phe Asn Lys Met Asn Ser Ile Tyr Arg Ser Leu Thr 195 200 205	624
aaa gat gaa gaa tta tta tat aaa tgt ttt act tat ttt tat aaa aaa Lys Asp Glu Glu Leu Leu Tyr Lys Cys Phe Thr Tyr Phe Tyr Lys Lys 210 215 220	672
tat ttt aaa aat att ttt aat gtt ata atg att aat aat tat tca tca Tyr Phe Lys Asn Ile Phe Asn Val Ile Met Ile Asn Asn Tyr Ser Ser 225 230 235 240	720
ata att tat tat tta agt act att aaa gat tta tta act aat aaa gat Ile Ile Tyr Tyr Leu Ser Thr Ile Lys Asp Leu Leu Thr Asn Lys Asp 245 250 255	768
tat aaa gac aaa ata tat gga tct att ata ata atg cct tta gct ata Tyr Lys Asp Lys Ile Tyr Gly Ser Ile Ile Ile Met Pro Leu Ala Ile 260 265 270	816
tgt gcg tcg aat gag ttg aaa ctt tca ata tat aat gac aca tat gtt Cys Ala Ser Asn Glu Leu Lys Leu Ser Ile Tyr Asn Asp Thr Tyr Val 275 280 285	864
cca gat atg ata aat gga aat att gca tat gaa gta aat aat aga tat Pro Asp Met Ile Asn Gly Asn Ile Ala Tyr Glu Val Asn Asn Arg Tyr 290 295 300	912
ata aga cat att gta tta gtt gtt tta tta tta ata tgt ata cca aac Ile Arg His Ile Val Leu Val Val Leu Leu Leu Ile Cys Ile Pro Asn 305 310 315 320	960
aaa gat aga atg ata ttt ttt cac aat gat ata aaa ccc aat aat ata Lys Asp Arg Met Ile Phe Phe His Asn Asp Ile Lys Pro Asn Asn Ile 325 330 335	1008
tta gtt ttt cct aat gta aat aaa gaa aaa tta ata ata aaa tat aac Leu Val Phe Pro Asn Val Asn Lys Glu Lys Leu Ile Ile Lys Tyr Asn 340 345 350	1056
aat agg aat ata ata ttt aaa gaa tta tat ata tta aaa tta aca gat Asn Arg Asn Ile Ile Phe Lys Glu Leu Tyr Ile Leu Lys Leu Thr Asp 355 360 365	1104
ttt gat tta tct aga ata gaa gga tta gat aac aat aga att aaa aat Phe Asp Leu Ser Arg Ile Glu Gly Leu Asp Asn Asn Arg Ile Lys Asn 370 375 380	1152
tct cca ata tta tta tat aat aac ata att aac gat ata tat tat ttt Ser Pro Ile Leu Leu Tyr Asn Asn Ile Ile Asn Asp Ile Tyr Tyr Phe 385 390 395 400	1200
ttt tat aga tta aaa tat gat ttt ttt tta aat tta aaa aca ata gat	1248



Phe	Tyr	Arg	Leu	Lys	Tyr	Asp	Phe	Phe	Leu	Asn	Leu	Lys	Thr	Ile	Asp	
				405					410					415		
cca	gag	tta	aac	gaa	cat	ata	gaa	aat	aaa	ttt	tta	tta	aaa	aaa	tat	1296
Pro	Glu	Leu	Asn	Glu	His	Ile	Glu	Asn	Lys	Phe	Leu	Leu	Lys	Lys	Tyr	
			420					425					430			
atg	aaa	gat	act	ata	aat	aat	cat	aat	tac	aaa	gga	aat	gaa	aaa	atg	1344
Met	Lys	Asp	Thr	Ile	Asn	Asn	His	Asn	Tyr	Lys	Gly	Asn	Glu	Lys	Met	
		435					440					445				
tct	ata	agt	ttt	gtt	aat	gat	ttc	ata	ttt	aat	tct	gga	tta	ttt	aat	1392
Ser	Ile	Ser	Phe	Val	Asn	Asp	Phe	Ile	Phe	Asn	Ser	Gly	Leu	Phe	Asn	
	450					455					460					
tat	tgg	tta	gat	taa												1407
Tyr	Trp	Leu	Asp													
465																

&lt;210&gt; 51

&lt;211&gt; 714

&lt;212&gt; DNA

&lt;213&gt; Amsacta moorei entomopoxvirus

&lt;220&gt;

&lt;221&gt; exon

&lt;222&gt; (1)..(714)

&lt;223&gt;

<400>	51															
atg	tcg	gac	gtc	gat	tat	gat	gat	gat	caa	ttg	gag	cct	agc	gat	gaa	48
Met	Ser	Asp	Val	Asp	Tyr	Asp	Asp	Asp	Gln	Leu	Glu	Pro	Ser	Asp	Glu	
1				5					10					15		
gaa	gat	atg	gat	gat	cta	gtg	tat	agt	gaa	gtt	tgt	gca	aat	gat	gaa	96
Glu	Asp	Met	Asp	Asp	Leu	Val	Tyr	Ser	Glu	Val	Cys	Ala	Asn	Asp	Glu	
			20					25					30			
tct	gac	gaa	tct	gaa	ata	aat	tta	tta	gat	gaa	ata	att	aac	gaa	gaa	144
Ser	Asp	Glu	Ser	Glu	Ile	Asn	Leu	Leu	Asp	Glu	Ile	Ile	Asn	Glu	Glu	
		35					40					45				
caa	gaa	atg	gaa	ata	att	aaa	aaa	ata	aaa	acc	aaa	gat	aaa	att	aaa	192
Gln	Glu	Met	Glu	Ile	Ile	Lys	Lys	Ile	Lys	Thr	Lys	Asp	Lys	Ile	Lys	
	50						55				60					

tat ttt aaa ggt aaa att ata gat atg aat aaa ata aat aaa gca aaa	240
Tyr Phe Lys Gly Lys Ile Ile Asp Met Asn Lys Ile Asn Lys Ala Lys	
65 70 75 80	
 gaa aaa tat tta tat aat ata aaa ttt aat gaa tta ttg tct ata ttt	288
Glu Lys Tyr Leu Tyr Asn Ile Lys Phe Asn Glu Leu Leu Ser Ile Phe	
85 90 95	
 cta aat tat act aat att tta caa agt ggt gga ttg cca tta tta gat	336
Leu Asn Tyr Thr Asn Ile Leu Gln Ser Gly Gly Leu Pro Leu Leu Asp	
100 105 110	
 gaa att aaa tta aaa aat aat tat aat att gaa tta ttt tca aat tct	384
Glu Ile Lys Leu Lys Asn Asn Tyr Asn Ile Glu Leu Phe Ser Asn Ser	
115 120 125	
 tct aca aca cca gaa aca gca gca atg ata atg tta ata att atg aat	432
Ser Thr Thr Pro Glu Thr Ala Ala Met Ile Met Leu Ile Ile Met Asn	
130 135 140	
 ata cct atg tgt gtt aaa aaa aac aat aaa ata tat aat aga gaa gta	480
Ile Pro Met Cys Val Lys Lys Asn Asn Lys Ile Tyr Asn Arg Glu Val	
145 150 155 160	
 tta aat ata gat aaa ttg aat atc gat tat ata aat tgt tat tac caa	528
Leu Asn Ile Asp Lys Leu Asn Ile Asp Tyr Ile Asn Cys Tyr Tyr Gln	
165 170 175	
 aat gta aaa aat atg tta cga tgt gtt aca tat aat tct aat aat aaa	576
Asn Val Lys Asn Met Leu Arg Cys Val Thr Tyr Asn Ser Asn Asn Lys	
180 185 190	
 ttt gat ttt aat aaa ttt aaa att tta ttt ccg tta ttt ata gaa tat	624
Phe Asp Phe Asn Lys Phe Lys Ile Leu Phe Pro Leu Phe Ile Glu Tyr	
195 200 205	
 ata aat cgt gat gaa att agt aat gaa gaa tta gat gaa att aaa aat	672
Ile Asn Arg Asp Glu Ile Ser Asn Glu Glu Leu Asp Glu Ile Lys Asn	
210 215 220	
 gtt aaa aga att ata aca aat tat gat tat gaa aat tta taa	714
Val Lys Arg Ile Ile Thr Asn Tyr Asp Tyr Glu Asn Leu	
225 230 235	

&lt;210&gt; 52

&lt;211&gt; 246

&lt;212&gt; DNA

&lt;213&gt; Amsacta moorei entomopoxvirus

&lt;220&gt;

<221> exon

<222> (1) .. (246)

<223>

<400> 52

atg	caa	ata	ttc	att	aaa	aca	tta	aca	ggt	aaa	aca	atc	aca	cta	gaa	48
Met	Gln	Ile	Phe	Ile	Lys	Thr	Leu	Thr	Gly	Lys	Thr	Ile	Thr	Leu	Glu	
1				5					10					15		

gta	gaa	agt	tca	gat	act	ata	tca	aat	att	aaa	aat	aaa	ata	caa	gat	96
Val	Glu	Ser	Ser	Asp	Thr	Ile	Ser	Asn	Ile	Lys	Asn	Lys	Ile	Gln	Asp	
			20					25					30			

aaa	gaa	gga	att	cct	ccg	gat	cag	caa	aga	ttg	att	ttt	gct	gga	aaa	144
Lys	Glu	Gly	Ile	Pro	Pro	Asp	Gln	Gln	Arg	Leu	Ile	Phe	Ala	Gly	Lys	
		35					40					45				

caa	tta	gat	gat	agc	aga	act	ctt	tca	gat	tat	aat	ata	tct	aaa	gaa	192
Gln	Leu	Asp	Asp	Ser	Arg	Thr	Leu	Ser	Asp	Tyr	Asn	Ile	Ser	Lys	Glu	
	50					55					60					

tct	act	tta	cat	ttg	gta	tta	aga	ctt	aga	ggt	gga	acg	aat	ata	aat	240
Ser	Thr	Leu	His	Leu	Val	Leu	Arg	Leu	Arg	Gly	Gly	Thr	Asn	Ile	Asn	
65					70					75				80		

tat	tag															246
Tyr																

<210> 53

<211> 2013

<212> DNA

<213> Amsacta moorei entomopoxvirus

<220>

<221> exon

<222> (1) .. (2013)

<223>

<400> 53

atg	aat	aaa	gtt	ata	tta	gat	gat	ttg	aga	aat	gat	aat	att	ccg	aac	48
Met	Asn	Lys	Val	Ile	Leu	Asp	Asp	Leu	Arg	Asn	Asp	Asn	Ile	Pro	Asn	

1	5	10	15	
aat att gct caa att ttg cct cat cag tta gca aca tta gat ttt tta				96
Asn Ile Ala Gln Ile Leu Pro His Gln Leu Ala Thr Leu Asp Phe Leu				
	20	25	30	
tat caa aaa tgt ata aat aat gct aat agt gtt tta ttg ttt cat aaa				144
Tyr Gln Lys Cys Ile Asn Asn Ala Asn Ser Val Leu Leu Phe His Lys				
	35	40	45	
atg ggt tct ggt aaa aca att att tct ctt ttg ttt agc ata tta ata				192
Met Gly Ser Gly Lys Thr Ile Ile Ser Leu Leu Phe Ser Ile Leu Ile				
	50	55	60	
tgt aat att aaa aaa gtt ata ata gta ttg cct agt tat agt ata tta				240
Cys Asn Ile Lys Lys Val Ile Ile Val Leu Pro Ser Tyr Ser Ile Leu				
65	70	75	80	
gaa atg tgg aaa caa aat tta tat aga tct tta att tta ctt cct aat				288
Glu Met Trp Lys Gln Asn Leu Tyr Arg Ser Leu Ile Leu Leu Pro Asn				
	85	90	95	
aaa gaa tat aat tta caa aat att gaa ttt aca act aga aca aaa tta				336
Lys Glu Tyr Asn Leu Gln Asn Ile Glu Phe Thr Thr Arg Thr Lys Leu				
	100	105	110	
aac gaa gat ata atg tta ata ggt aaa act gat ata ata aat gaa aaa				384
Asn Glu Asp Ile Met Leu Ile Gly Lys Thr Asp Ile Ile Asn Glu Lys				
	115	120	125	
tta aaa aat tat aac gat tat att atg ata ata gat gaa gca cat aat				432
Leu Lys Asn Tyr Asn Asp Tyr Ile Met Ile Ile Asp Glu Ala His Asn				
	130	135	140	
ttt ttt gga aat atg aca ggt agt gta tta tct act cta aga aaa aat				480
Phe Phe Gly Asn Met Thr Gly Ser Val Leu Ser Thr Leu Arg Lys Asn				
145	150	155	160	
aca aat ata ata tat gtt tta ttg aca ggt agt ccg ata aca aat act				528
Thr Asn Ile Ile Tyr Val Leu Leu Thr Gly Ser Pro Ile Thr Asn Thr				
	165	170	175	
gtt tcg aca ata aaa gat att gtg gaa tta tta act agg gaa aca ttt				576
Val Ser Thr Ile Lys Asp Ile Val Glu Leu Leu Thr Arg Glu Thr Phe				
	180	185	190	
gat gaa aat aag tat att aaa ata ggt gga aat cgt gtt ttt gaa aaa				624
Asp Glu Asn Lys Tyr Ile Lys Ile Gly Gly Asn Arg Val Phe Glu Lys				
	195	200	205	
agt ata aat aac gaa ggt att gca ttt tta aat aaa aat cta aag ggt				672
Ser Ile Asn Asn Glu Gly Ile Ala Phe Leu Asn Lys Asn Leu Lys Gly				
	210	215	220	
tta ata tca tat tat gat gaa gag agg aaa gat gtt cct gaa gta aaa				720
Leu Ile Ser Tyr Tyr Asp Glu Glu Arg Lys Asp Val Pro Glu Val Lys				
225	230	235	240	

tac aga ggt aaa aaa ata ttt cta tgt cct ttg aca tta tgt cca atg	768
Tyr Arg Gly Lys Lys Ile Phe Leu Cys Pro Leu Thr Leu Cys Pro Met	
245 250 255	
tct aaa tta cat gaa gaa aat tat tat gaa gta gct aga aat act aaa	816
Ser Lys Leu His Glu Glu Asn Tyr Tyr Glu Val Ala Arg Asn Thr Lys	
260 265 270	
aat gat atg ttt gtt aaa tta tta atg agt gtt tcg ttg gtt gca tta	864
Asn Asp Met Phe Val Lys Leu Leu Met Ser Val Ser Leu Val Ala Leu	
275 280 285	
gga tct ata tca aat tat gaa aat ttt tca caa ttt atg gag aca gat	912
Gly Ser Ile Ser Asn Tyr Glu Asn Phe Ser Gln Phe Met Glu Thr Asp	
290 295 300	
aaa aaa ata ttt gat aat ttt tat att tct aat gga aaa ttt tca gga	960
Lys Lys Ile Phe Asp Asn Phe Tyr Ile Ser Asn Gly Lys Phe Ser Gly	
305 310 315 320	
tct gaa tta gtt aca tta aat ata tct tct aaa tta aaa act ttt aga	1008
Ser Glu Leu Val Thr Leu Asn Ile Ser Ser Lys Leu Lys Thr Phe Arg	
325 330 335	
gat act ata ttt aaa gaa aga aat gtt ggt aaa cga ttt gta tat ttt	1056
Asp Thr Ile Phe Lys Glu Arg Asn Val Gly Lys Arg Phe Val Tyr Phe	
340 345 350	
gct aat agt act ata gga agt gct ata ata aga agt gtt atg tta gca	1104
Ala Asn Ser Thr Ile Gly Ser Ala Ile Ile Arg Ser Val Met Leu Ala	
355 360 365	
aat ggc ata tct gaa tat gga aaa gaa att gtt aat aat ttt aca tgt	1152
Asn Gly Ile Ser Glu Tyr Gly Lys Glu Ile Val Asn Asn Phe Thr Cys	
370 375 380	
gtt aat tgt ata aag gat aaa att tgt cac aat gga gaa tgt att cct	1200
Val Asn Cys Ile Lys Asp Lys Ile Cys His Asn Gly Glu Cys Ile Pro	
385 390 395 400	
atg aga ttt gta ata att aca tca aaa gaa tta aat aaa gga aat agt	1248
Met Arg Phe Val Ile Ile Thr Ser Lys Glu Leu Asn Lys Gly Asn Ser	
405 410 415	
aat tat ata aat aat att tta agt att ttt aac gaa gat att aat gat	1296
Asn Tyr Ile Asn Asn Ile Leu Ser Ile Phe Asn Glu Asp Ile Asn Asp	
420 425 430	
gat gga aat aat ata atg ttt tta ttt ggt tca aaa att ata tca gaa	1344
Asp Gly Asn Asn Ile Met Phe Leu Phe Gly Ser Lys Ile Ile Ser Glu	
435 440 445	
gct tat act tta aaa aac gta aaa gat ata tgg ttt tta act gtt cct	1392
Ala Tyr Thr Leu Lys Asn Val Lys Asp Ile Trp Phe Leu Thr Val Pro	
450 455 460	

gaa aca aaa tct gaa tta gat caa tgt gta gct aga gct gtt aga tca	1440
Glu Thr Lys Ser Glu Leu Asp Gln Cys Val Ala Arg Ala Val Arg Ser	
465 470 475 480	
ttt tct tat aaa gat act aat aca aaa gta ata att aga ata tgt att	1488
Phe Ser Tyr Lys Asp Thr Asn Thr Lys Val Ile Ile Arg Ile Cys Ile	
485 490 495	
gca tca aca aca aat aca tta agt aac gat gtt tct aaa aca att gaa	1536
Ala Ser Thr Thr Asn Thr Leu Ser Asn Asp Val Ser Lys Thr Ile Glu	
500 505 510	
caa tat aaà gat gtt aat att tct gat gtt tat aaa aat act tta tta	1584
Gln Tyr Lys Asp Val Asn Ile Ser Asp Val Tyr Lys Asn Thr Leu Leu	
515 520 525	
aat aaa att gaa tta ttg tta acg gaa agt tcg tat act tta tct tat	1632
Asn Lys Ile Glu Leu Leu Leu Thr Glu Ser Ser Tyr Thr Leu Ser Tyr	
530 535 540	
gat ttt aga aaa caa tta tat tct gaa tta aaa ttt gaa aaa tct aaa	1680
Asp Phe Arg Lys Gln Leu Tyr Ser Glu Leu Lys Phe Glu Lys Ser Lys	
545 550 555 560	
gta gct gat aat ata ttt aaa aat cta act att tta tct tca gat acc	1728
Val Ala Asp Asn Ile Phe Lys Asn Leu Thr Ile Leu Ser Ser Asp Thr	
565 570 575	
atc gag agt gat gtt ttg gaa tgt ttt gtt tta gaa aaa atc cga aga	1776
Ile Glu Ser Asp Val Leu Glu Cys Phe Val Leu Glu Lys Ile Arg Arg	
580 585 590	
tat tgt tat tac aat aca aga ttt aaa ttt aca aca tta aac gaa tat	1824
Tyr Cys Tyr Tyr Asn Thr Arg Phe Lys Phe Thr Thr Leu Asn Glu Tyr	
595 600 605	
ata att aaa aat ata gat att aaa tat aat gat aaa ata aaa gaa tat	1872
Ile Ile Lys Asn Ile Asp Ile Lys Tyr Asn Asp Lys Ile Lys Glu Tyr	
610 615 620	
att aat aat gct ata gaa tca tca ttt gtt ata gaa aat gat ata ttt	1920
Ile Asn Asn Ala Ile Glu Ser Ser Phe Val Ile Glu Asn Asp Ile Phe	
625 630 635 640	
ggt aat tgc tat tta aca tat ttt aaa aat gat att gtt acg gtt ccc	1968
Gly Asn Cys Tyr Leu Thr Tyr Phe Lys Asn Asp Ile Val Thr Val Pro	
645 650 655	
ata gta tta gaa tat aat aat cat cta tta tca gtt aga ttg tga	2013
Ile Val Leu Glu Tyr Asn Asn His Leu Leu Ser Val Arg Leu	
660 665 670	

&lt;210&gt; 54

&lt;211&gt; 1395

&lt;212&gt; DNA

&lt;213&gt; Amsacta moorei entomopoxvirus

&lt;220&gt;

&lt;221&gt; exon

&lt;222&gt; (1) .. (1395)

&lt;223&gt;

&lt;400&gt; 54

atg aat aat aaa att aga aga ttt cca aat aaa aat tta aaa atg cca	48
Met Asn Asn Lys Ile Arg Arg Phe Pro Asn Lys Asn Leu Lys Met Pro	
1 5 10 15	
 gaa tct ggt att aat ttt atg tct atg tta ttt ttt agt aaa ata gat	96
Glu Ser Gly Ile Asn Phe Met Ser Met Leu Phe Phe Ser Lys Ile Asp	
20 25 30	
 aat atg gta tat ttt ata aat cct att aaa tat aat act aat gca aat	144
Asn Met Val Tyr Phe Ile Asn Pro Ile Lys Tyr Asn Thr Asn Ala Asn	
35 40 45	
 ata gct ata tta gaa aaa ata gat gat gat gat gaa aca aga ggt aaa	192
Ile Ala Ile Leu Glu Lys Ile Asp Asp Asp Asp Glu Thr Arg Gly Lys	
50 55 60	
 gta aca ttt ata cct ata aaa tac ttg gaa ata tta tat aat gaa tta	240
Val Thr Phe Ile Pro Ile Lys Tyr Leu Glu Ile Leu Tyr Asn Glu Leu	
65 70 75 80	
 gtt tta gat cca aat cat att aat aat att aat ttt gaa aat aat att	288
Val Leu Asp Pro Asn His Ile Asn Asn Ile Asn Phe Glu Asn Asn Ile	
85 90 95	
 aaa aga aaa ttt ttt cta ttt tgg act ata aaa aaa tat tta caa gat	336
Lys Arg Lys Phe Phe Leu Phe Trp Thr Ile Lys Lys Tyr Leu Gln Asp	
100 105 110	
 aaa aat ata aat att aat act ttt att aca tct aaa aaa tat aaa ggc	384
Lys Asn Ile Asn Ile Asn Thr Phe Ile Thr Ser Lys Lys Tyr Lys Gly	
115 120 125	
 att cca tta gta tat atg aga aag tct ttt cta aaa tca gaa tta tcc	432
Ile Pro Leu Val Tyr Met Arg Lys Ser Phe Leu Lys Ser Glu Leu Ser	
130 135 140	
 aaa aca aga gat ttt tct aca ttt gcc aca att tat gat gat ttg gat	480
Lys Thr Arg Asp Phe Ser Thr Phe Ala Thr Ile Tyr Asp Asp Leu Asp	
145 150 155 160	

gct caa ata gga ata ccg cct ttg gga ttt aat cct aaa cct aaa gct	528
Ala Gln Ile Gly Ile Pro Pro Leu Gly Phe Asn Pro Lys Pro Lys Ala	
165 170 175	
tac cca aga aaa cat gat aaa tct aca tgg tta agt tcg gga gat ata	576
Tyr Pro Arg Lys His Asp Lys Ser Thr Trp Leu Ser Ser Gly Asp Ile	
180 185 190	
tat aat tgt ata tat cca tta act atg att aat aca gat tat gat tat	624
Tyr Asn Cys Ile Tyr Pro Leu Thr Met Ile Asn Thr Asp Tyr Asp Tyr	
195 200 205	
ttt cat ttg att tta ttt gaa aaa act gat aaa aat att gct aca gta	672
Phe His Leu Ile Leu Phe Glu Lys Thr Asp Lys Asn Ile Ala Thr Val	
210 215 220	
gct tca tct atg aga tgc tat aaa ctt gaa gat aga gta aaa ttt ttt	720
Ala Ser Ser Met Arg Cys Tyr Lys Leu Glu Asp Arg Val Lys Phe Phe	
225 230 235 240	
tta atg aat gat aaa aaa aga ttt ttt atg ttt cct ata att tat aat	768
Leu Met Asn Asp Lys Lys Arg Phe Phe Met Phe Pro Ile Ile Tyr Asn	
245 250 255	
gat cat ttt act tgt tgc gta ata gat aaa cac ttt gat aaa gat aaa	816
Asp His Phe Thr Cys Cys Val Ile Asp Lys His Phe Asp Lys Asp Lys	
260 265 270	
aaa gct gca tac ttt ttt aat agt agt ggt tat ata cca gaa ctt ata	864
Lys Ala Ala Tyr Phe Phe Asn Ser Ser Gly Tyr Ile Pro Glu Leu Ile	
275 280 285	
aaa caa aat aaa aaa tat atg ttt att gaa tct gat atg act ata aaa	912
Lys Gln Asn Lys Lys Tyr Met Phe Ile Glu Ser Asp Met Thr Ile Lys	
290 295 300	
agc cat aaa cac tac aat agt act cct aat act aat tat gct tat tta	960
Ser His Lys His Tyr Asn Ser Thr Pro Asn Thr Asn Tyr Ala Tyr Leu	
305 310 315 320	
tac att gat gta cta tca gaa tat tta aat gat ata ttt aaa aat gta	1008
Tyr Ile Asp Val Leu Ser Glu Tyr Leu Asn Asp Ile Phe Lys Asn Val	
325 330 335	
aat tat tac ttt ttt aat act ttt gaa tta caa tat gat agt ccc gat	1056
Asn Tyr Tyr Phe Phe Asn Thr Phe Glu Leu Gln Tyr Asp Ser Pro Asp	
340 345 350	
tgt ggt atg ttt aat ata ata ttt tta tat tat ata gtt tat ttc aac	1104
Cys Gly Met Phe Asn Ile Ile Phe Leu Tyr Tyr Ile Val Tyr Phe Asn	
355 360 365	
ata aaa tct aaa ttt gaa ttt aaa aaa tta tat tat tct atg agt ttt	1152
Ile Lys Ser Lys Phe Glu Phe Lys Lys Leu Tyr Tyr Ser Met Ser Phe	
370 375 380	
att ggt gat tta ttg gct agt agt tat aga ggt gca tta ttt att tct	1200



ata gga tta aaa aat ttg aat agt atg tta tta ttt tgg gat act ggt 192  
Ile Gly Leu Lys Asn Leu Asn Ser Met Leu Leu Phe Trp Asp Thr Gly

50	55	60	
atg gga aaa aca tta act gct gtg tat att ata aaa tat ata aaa gaa Met Gly Lys Thr Leu Thr Ala Val Tyr Ile Ile Lys Tyr Ile Lys Glu 65 70 75 80			240
tta ttt cca aga tgg ata att tta ata ttt att aaa aaa tca tta tac Leu Phe Pro Arg Trp Ile Ile Leu Ile Phe Ile Lys Lys Ser Leu Tyr 85 90 95			288
ata gat cct tgg tta aat act ata aga tca tat ata tca gat acc agt Ile Asp Pro Trp Leu Asn Thr Ile Arg Ser Tyr Ile Ser Asp Thr Ser 100 105 110			336
aat ata aaa ttt ata tat tat gat tgc tca tct agt tta gat aaa ttt Asn Ile Lys Phe Ile Tyr Tyr Asp Ser Ser Ser Ser Leu Asp Lys Phe 115 120 125			384
aat aat ata tat aga tct ata gaa agt tct ctt aat aaa aaa agt aga Asn Asn Ile Tyr Arg Ser Ile Glu Ser Ser Leu Asn Lys Lys Ser Arg 130 135 140			432
tta cta ata ata ata gac gaa gtt cat aaa tta ata tca aga act gtt Leu Leu Ile Ile Ile Asp Glu Val His Lys Leu Ile Ser Arg Thr Val 145 150 155 160			480
aaa aaa gat aat aac gaa aga aat ttt act cct att tat aaa aaa tta Lys Lys Asp Asn Asn Glu Arg Asn Phe Thr Pro Ile Tyr Lys Lys Leu 165 170 175			528
ata aaa tta gca aat ttc gaa aat aat aaa ata tta tgt atg tcc gct Ile Lys Leu Ala Asn Phe Glu Asn Asn Lys Ile Leu Cys Met Ser Ala 180 185 190			576
act cca gta act aat aat att tct gaa ttt aat aat tta ata ggt tta Thr Pro Val Thr Asn Asn Ile Ser Glu Phe Asn Asn Leu Ile Gly Leu 195 200 205			624
ctt aga cca aat gtt atg aat ata aaa gaa gaa tat ata aat aat gga Leu Arg Pro Asn Val Met Asn Ile Lys Glu Glu Tyr Ile Asn Asn Gly 210 215 220			672
aag tta att aat ttt aag gaa tta aga gaa aca tta tta gct ata tgt Lys Leu Ile Asn Phe Lys Glu Leu Arg Glu Thr Leu Leu Ala Ile Cys 225 230 235 240			720
tct tat aaa aga tta ata gaa gca gat agt tta aca gaa aca aat tat Ser Tyr Lys Arg Leu Ile Glu Ala Asp Ser Leu Thr Glu Thr Asn Tyr 245 250 255			768
ata gat gga tat gca aaa aaa aat ata ttt tat cat aat ata att atg Ile Asp Gly Tyr Ala Lys Lys Asn Ile Phe Tyr His Asn Ile Ile Met 260 265 270			816
tca gat gag caa tct aaa tta tat aat atg gca gaa aaa tat gat tat Ser Asp Glu Gln Ser Lys Leu Tyr Asn Met Ala Glu Lys Tyr Asp Tyr 275 280 285			864

aaa act gaa tta ggt ggt tta aaa act atg aga aga tta ata tct tca	912
Lys Thr Glu Leu Gly Gly Leu Lys Thr Met Arg Arg Leu Ile Ser Ser	
290 325 300	
ttt gct ttt tat gat ctt aaa ata aaa gga gat tta gat aat ata gaa	960
Phe Ala Phe Tyr Asp Leu Lys Ile Lys Gly Asp Leu Asp Asn Ile Glu	
305 310 315 320	
tat aat gat atg att aaa aga aaa ctt gct gaa ttt tcc gag ttt aca	1008
Tyr Asn Asp Met Ile Lys Arg Lys Leu Ala Glu Phe Ser Glu Phe Thr	
325 330 335	
aaa aat att aat ttc tct gaa tct ttt att gaa agt ttt aaa aat gat	1056
Lys Asn Ile Asn Phe Ser Glu Ser Phe Ile Glu Ser Phe Lys Asn Asp	
340 345 350	
aat ata aaa ata aaa act aat tta cca atc act gat ata aat aat tat	1104
Asn Ile Lys Ile Lys Thr Asn Leu Pro Ile Thr Asp Ile Asn Asn Tyr	
355 360 365	
aat ata tta tat caa tat tcg tgt aaa tat ata gaa act tgt aaa ata	1152
Asn Ile Leu Tyr Gln Tyr Ser Cys Lys Tyr Ile Glu Thr Cys Lys Ile	
370 375 380	
att tta aat tcg aga gga aaa gta tta ata ttt gaa cct tta gtt aat	1200
Ile Leu Asn Ser Arg Gly Lys Val Leu Ile Phe Glu Pro Leu Val Asn	
385 390 395 400	
ttt gaa gga ata tca agt tta aaa tgt tat ttt aat tgt ttt aat att	1248
Phe Glu Gly Ile Ser Ser Leu Lys Cys Tyr Phe Asn Cys Phe Asn Ile	
405 410 415	
tct tat att gaa tat tct agc aaa act tta aaa act aga gat aat gaa	1296
Ser Tyr Ile Glu Tyr Ser Ser Lys Thr Leu Lys Thr Arg Asp Asn Glu	
420 425 430	
tta aac gaa tat aat aat tat gaa aat aat aat ggt aaa aaa gta aaa	1344
Leu Asn Glu Tyr Asn Asn Tyr Glu Asn Asn Asn Gly Lys Lys Val Lys	
435 440 445	
gtt tgc ata ttt tct tac gct gga tct gaa ggc ata tca ttc aaa tgt	1392
Val Cys Ile Phe Ser Tyr Ala Gly Ser Glu Gly Ile Ser Phe Lys Cys	
450 455 460	
att aat gat ata att ata tta gat atg ccg tgg aat gaa tca gaa tta	1440
Ile Asn Asp Ile Ile Ile Leu Asp Met Pro Trp Asn Glu Ser Glu Leu	
465 470 475 480	
aaa caa ata ata gga aga tct ata aga tta aat tct cat aaa gat tta	1488
Lys Gln Ile Ile Gly Arg Ser Ile Arg Leu Asn Ser His Lys Asp Leu	
485 490 495	
cca caa gaa tat aga tat gtt aac gtt cat ttt tta ata tca tat acc	1536
Pro Gln Glu Tyr Arg Tyr Val Asn Val His Phe Leu Ile Ser Tyr Thr	
500 505 510	

aac aac aga aaa tct gta gat aaa gaa ata tta gat att ata aaa gat	1584
Asn Asn Arg Lys Ser Val Asp Lys Glu Ile Leu Asp Ile Ile Lys Asp	
515 520 525	
aaa caa ggt aaa ata aat gtt ata ttt gat tta tta aaa tca tca tct	1632
Lys Gln Gly Lys Ile Asn Val Ile Phe Asp Leu Leu Lys Ser Ser Ser	
530 535 540	
atc gaa tct att cat aac aca tat aaa tat ata gaa cca gca gaa aat	1680
Ile Glu Ser Ile His Asn Thr Tyr Lys Tyr Ile Glu Pro Ala Glu Asn	
545 550 555 560	
gaa ata att ttt gac aca ata cgt aaa act aga atg aaa gaa atg aac	1728
Glu Ile Ile Phe Asp Thr Ile Arg Lys Thr Arg Met Lys Glu Met Asn	
565 570 575	
gta tct aat gtt att att aat ata aaa tta tat ccc ata tca tat tgt	1776
Val Ser Asn Val Ile Ile Asn Ile Lys Leu Tyr Pro Ile Ser Tyr Cys	
580 585 590	
aaa gat tat gat aga gcc act ata tta aaa ggt tta tta aac aaa gac	1824
Lys Asp Tyr Asp Arg Ala Thr Ile Leu Lys Gly Leu Leu Asn Lys Asp	
595 600 605	
aca aat ata gta tat aaa gat aat aca gct gta gca aaa tta atg att	1872
Thr Asn Ile Val Tyr Lys Asp Asn Thr Ala Val Ala Lys Leu Met Ile	
610 615 620	
gat aaa gac aat ata cct ata ttt ata ata gag aat gat aca tta ata	1920
Asp Lys Asp Asn Ile Pro Ile Phe Ile Ile Glu Asn Asp Thr Leu Ile	
625 630 635 640	
tat ata gca gat gat tat tat gaa tag	1947
Tyr Ile Ala Asp Asp Tyr Tyr Glu	
645	

&lt;210&gt; 56

&lt;211&gt; 453

&lt;212&gt; DNA

&lt;213&gt; Amsacta moorei entomopoxvirus

&lt;220&gt;

&lt;221&gt; exon

&lt;222&gt; (1) .. (453)

&lt;223&gt;

&lt;400&gt; 56

atg aac gta aaa att ata gaa aaa tat caa cat ttt aaa gaa gat aaa 48  
 Met Asn Val Lys Ile Ile Glu Lys Tyr Gln His Phe Lys Glu Asp Lys  
 1 5 10 15

tat ata tca tat tat aat ata ttt ata tat ata cta gaa gaa tat att 96  
 Tyr Ile Ser Tyr Tyr Asn Ile Phe Ile Tyr Ile Leu Glu Glu Tyr Ile  
 20 25 30

ata ata tta tat aat tat aaa tta ata tat ata ata aat aaa aat tat 144  
 Ile Ile Leu Tyr Asn Tyr Lys Leu Ile Tyr Ile Ile Asn Lys Asn Tyr  
 35 40 45

ata caa tat atg tat tat aat tat tta ttt aaa aat aat ata tat tat 192  
 Ile Gln Tyr Met Tyr Tyr Asn Tyr Leu Phe Lys Asn Asn Ile Tyr Tyr  
 50 55 60

aat tta aaa tta tat aat aat aat aaa tta tta aaa cat aaa ccg tcg 240  
 Asn Leu Lys Leu Tyr Asn Asn Asn Lys Leu Leu Lys His Lys Pro Ser  
 65 70 75 80

aaa aaa gta cgc ttt tca tcc gaa cca cca aaa ctc cac att atg tat 288  
 Lys Lys Val Arg Phe Ser Ser Glu Pro Pro Lys Leu His Ile Met Tyr  
 85 90 95

gtt tgg tta tat gct gca aaa caa act cga aaa tta tac tgg gat aaa 336  
 Val Trp Leu Tyr Ala Ala Lys Gln Thr Arg Lys Leu Tyr Trp Asp Lys  
 100 105 110

ttt gcg att gat aga cat aga ttc aaa aga aga att aat gat ata gat 384  
 Phe Ala Ile Asp Arg His Arg Phe Lys Arg Arg Ile Asn Asp Ile Asp  
 115 120 125

ata tca ata tct tgg gtt tta act cca cat cac aga cat aaa att atg 432  
 Ile Ser Ile Ser Trp Val Leu Thr Pro His His Arg His Lys Ile Met  
 130 135 140

aaa cat ctt aag tta ata taa 453  
 Lys His Leu Lys Leu Ile  
 145 150

&lt;210&gt; 57

&lt;211&gt; 900

&lt;212&gt; DNA

&lt;213&gt; Amsacta moorei entomopoxvirus

&lt;220&gt;

&lt;221&gt; exon

&lt;222&gt; (1) .. (900)

&lt;223&gt;

&lt;400&gt; 57

atg gac gaa aca ata aat ttt aat aat aaa tca tgg gaa ata aaa aat	48
Met Asp Glu Thr Ile Asn Phe Asn Asn Lys Ser Trp Glu Ile Lys Asn	
1 5 10 15	
tta ata gct aaa ggt ggt ttt gga aca gta tat aaa tta tgc gaa aaa	96
Leu Ile Ala Lys Gly Gly Phe Gly Thr Val Tyr Lys Leu Cys Glu Lys	
20 25 30	
aat gat aat aat aac tgt tac gct att aaa ata gaa cca tcg gat aat	144
Asn Asp Asn Asn Asn Cys Tyr Ala Ile Lys Ile Glu Pro Ser Asp Asn	
35 40 45	
ggt ccg ttg ttt gta gaa atg cac ttt tat aaa aaa ata aat aaa aat	192
Gly Pro Leu Phe Val Glu Met His Phe Tyr Lys Lys Ile Asn Lys Asn	
50 55 60	
gaa ata aaa aat ttt att gat gcg aaa aat tta agt tat tta gga ata	240
Glu Ile Lys Asn Phe Ile Asp Ala Lys Asn Leu Ser Tyr Leu Gly Ile	
65 70 75 80	
cca tta cta tat cat aat ggt att ata aaa aaa gat aat ata gaa tat	288
Pro Leu Leu Tyr His Asn Gly Ile Ile Lys Lys Asp Asn Ile Glu Tyr	
85 90 95	
aga tat ata gta ata gat tat tat gaa ttt aat tta aat gat ata tta	336
Arg Tyr Ile Val Ile Asp Tyr Tyr Glu Phe Asn Leu Asn Asp Ile Leu	
100 105 110	
aaa aaa tat ata aaa tta cct ata ata aca ata tat aaa ata act ata	384
Lys Lys Tyr Ile Lys Leu Pro Ile Ile Thr Ile Tyr Lys Ile Thr Ile	
115 120 125	
caa ata tta tat ata tta gaa tat tta cac aaa aaa aaa tat aca cac	432
Gln Ile Leu Tyr Ile Leu Glu Tyr Leu His Lys Lys Lys Tyr Thr His	
130 135 140	
aat gat ata aaa aaa aat aat ata atg ttt aat tca tca tta act aaa	480
Asn Asp Ile Lys Lys Asn Asn Ile Met Phe Asn Ser Ser Leu Thr Lys	
145 150 155 160	
gta tat tta ata gat tac gga cta ata tat aat atg aat tct aat caa	528
Val Tyr Leu Ile Asp Tyr Gly Leu Ile Tyr Asn Met Asn Ser Asn Gln	
165 170 175	
gaa tat aat ata aaa tgt agt aat gat gga act cta gaa tat tta cca	576
Glu Tyr Asn Ile Lys Cys Ser Asn Asp Gly Thr Leu Glu Tyr Leu Pro	
180 185 190	
tta ata act cat tta ttt ggc tta aaa aca tac atg gga gat ata gag	624
Leu Ile Thr His Leu Phe Gly Leu Lys Thr Tyr Met Gly Asp Ile Glu	

195	200	205	
tct ctg atg tat aat att att gaa tgg tat agt gga agt ttg cct tgg			672
Ser Leu Met Tyr Asn Ile Ile Glu Trp Tyr Ser Gly Ser Leu Pro Trp			
210	215	220	
att aaa tat aaa aaa aaa aat gtt ata tta aaa aaa tta gat ttt ttc			720
Ile Lys Tyr Lys Lys Lys Asn Val Ile Leu Lys Lys Leu Asp Phe Phe			
225	230	235	240
aac act tgt tta act aat tca cca att gaa ata tgt aaa tta tat aat			768
Asn Thr Cys Leu Thr Asn Ser Pro Ile Glu Ile Cys Lys Leu Tyr Asn			
245	250	255	
tat ata aaa aat gct cct tct ata tat aat tat aat ttt ata cct gat			816
Tyr Ile Lys Asn Ala Pro Ser Ile Tyr Asn Tyr Asn Phe Ile Pro Asp			
260	265	270	
cat gat aaa tta att aat tat ttt gta act tat tta aaa tct aaa aat			864
His Asp Lys Leu Ile Asn Tyr Phe Val Thr Tyr Leu Lys Ser Lys Asn			
275	280	285	
ata aat tta aat gat aaa tta gtt ttt tgt aaa taa			900
Ile Asn Leu Asn Asp Lys Leu Val Phe Cys Lys			
290	295		

&lt;210&gt; 58

&lt;211&gt; 1599

&lt;212&gt; DNA

&lt;213&gt; Amsacta moorei entomopoxvirus

&lt;220&gt;

&lt;221&gt; exon

&lt;222&gt; (1) .. (1599)

&lt;223&gt;

&lt;400&gt; 58

atg aat cat att aaa aaa att tta aaa ata aaa agt gat aaa gat ata	48
Met Asn His Ile Lys Lys Ile Leu Lys Ile Lys Ser Asp Lys Asp Ile	
1 5 10 15	

tta aat tac ata gat gca tta aat tat aat gat tta gaa aat ata ata	96
Leu Asn Tyr Ile Asp Ala Leu Asn Tyr Asn Asp Leu Glu Asn Ile Ile	
20 25 30	

cag aca tta gat aat agt tat tat gat aaa gaa gct tta att agt gat	144
-----------------------------------------------------------------	-----

Gln	Thr	Leu	Asp	Asn	Ser	Tyr	Tyr	Asp	Lys	Glu	Ala	Leu	Ile	Ser	Asp		
		35					40					45					
aaa	aaa	tat	gat	tta	ata	aga	aat	ttt	ata	aat	aat	aag	tat	cct	aat	192	
Lys	Lys	Tyr	Asp	Leu	Ile	Arg	Asn	Phe	Ile	Asn	Asn	Lys	Tyr	Pro	Asn		
	50					55				60							
gaa	tct	ttg	tgt	aaa	aaa	ata	ggg	tat	act	ccg	gaa	gat	aaa	gta	cga	240	
Glu	Ser	Leu	Cys	Lys	Lys	Ile	Gly	Tyr	Thr	Pro	Glu	Asp	Lys	Val	Arg		
65					70				75					80			
tta	aag	tat	ttt	atg	ggg	agt	gaa	aat	aaa	act	tat	aaa	tca	gat	aat	288	
Leu	Lys	Tyr	Phe	Met	Gly	Ser	Glu	Asn	Lys	Thr	Tyr	Lys	Ser	Asp	Asn		
				85				90						95			
aaa	tta	tta	agt	tgg	ata	aac	gaa	tat	cat	act	aat	ata	tta	gta	tta	336	
Lys	Leu	Leu	Ser	Trp	Ile	Asn	Glu	Tyr	His	Thr	Asn	Ile	Leu	Val	Leu		
			100					105					110				
tct	gca	aaa	gca	gac	gga	ata	tca	gta	tta	tgg	gat	ata	aaa	aat	aat	384	
Ser	Ala	Lys	Ala	Asp	Gly	Ile	Ser	Val	Leu	Trp	Asp	Ile	Lys	Asn	Asn		
		115						120				125					
aaa	ata	tat	agt	aga	ggg	gat	ggg	aaa	tat	gga	aaa	gat	ata	aca	cat	432	
Lys	Ile	Tyr	Ser	Arg	Gly	Asp	Gly	Lys	Tyr	Gly	Lys	Asp	Ile	Thr	His		
	130					135					140						
ttt	att	aat	tat	ttt	aat	ttt	tca	gat	gat	aaa	aat	ata	aat	aac	aat	480	
Phe	Ile	Asn	Tyr	Phe	Asn	Phe	Ser	Asp	Asp	Lys	Asn	Ile	Asn	Asn	Asn		
145					150					155					160		
gat	ata	ttt	aaa	aat	aat	ata	aat	ttt	gtt	aga	ggg	gaa	tta	gtt	ata	528	
Asp	Ile	Phe	Lys	Asn	Asn	Ile	Asn	Phe	Val	Arg	Gly	Glu	Leu	Val	Ile		
				165					170					175			
gat	aaa	cct	gaa	aat	aga	aat	ata	gta	gca	ggg	caa	ata	aat	aga	aat	576	
Asp	Lys	Pro	Glu	Asn	Arg	Asn	Ile	Val	Ala	Gly	Gln	Ile	Asn	Arg	Asn		
			180					185					190				
gaa	att	gat	aaa	gaa	acc	gca	tta	aaa	ata	tat	ttt	gta	gca	tac	gaa	624	
Glu	Ile	Asp	Lys	Glu	Thr	Ala	Leu	Lys	Ile	Tyr	Phe	Val	Ala	Tyr	Glu		
		195					200					205					
ata	tta	gaa	cca	aga	atg	aca	caa	ctc	gaa	caa	ttt	cac	aaa	ctt	aca	672	
Ile	Leu	Glu	Pro	Arg	Met	Thr	Gln	Leu	Glu	Gln	Phe	His	Lys	Leu	Thr		
	210					215					220						
gag	aat	agt	ata	aga	act	gtt	aaa	tat	gat	tct	gtt	gat	tat	aat	att	720	
Glu	Asn	Ser	Ile	Arg	Thr	Val	Lys	Tyr	Asp	Ser	Val	Asp	Tyr	Asn	Ile		
225					230					235					240		
tca	tac	gaa	caa	tta	agt	gaa	ata	tat	aat	aat	tat	acg	caa	gaa	tta	768	
Ser	Tyr	Glu	Gln	Leu	Ser	Glu	Ile	Tyr	Asn	Asn	Tyr	Thr	Gln	Glu	Leu		
				245					250					255			
tcg	tat	tac	ata	gat	ggg	att	ata	ata	aga	aat	aat	aat	tta	aat	cca	816	
Ser	Tyr	Tyr	Ile	Asp	Gly	Ile	Ile	Ile	Arg	Asn	Asn	Asn	Leu	Asn	Pro		



260	265	270	
gtt att aaa tct ggt aat cca cct tgg tca ata tgt ttt aag gaa aca Val Ile Lys Ser Gly Asn Pro Pro Trp Ser Ile Cys Phe Lys Glu Thr 275 280 285			864
gat aaa ata tat att act act gtt aaa gaa atc aaa tgg gat ata tca Asp Lys Ile Tyr Ile Thr Thr Val Lys Glu Ile Lys Trp Asp Ile Ser 290 295 300			912
aaa aaa aat ata tat ata cct aaa gca ata tta gag cct ata att ata Lys Lys Asn Ile Tyr Ile Pro Lys Ala Ile Leu Glu Pro Ile Ile Ile 305 310 315 320			960
gat aat tcg act att aat gct gtt gct tgt cac aat gct aaa tat gta Asp Asn Ser Thr Ile Asn Ala Val Ala Cys His Asn Ala Lys Tyr Val 325 330 335			1008
att gat aaa aaa att aac act ggt tca ata gta gaa ata gta aag aaa Ile Asp Lys Lys Ile Asn Thr Gly Ser Ile Val Glu Ile Val Lys Lys 340 345 350			1056
ggg gga gtt ata ccg ata att aat aat gta ata aaa gaa tca gat ata Gly Gly Val Ile Pro Ile Ile Asn Asn Val Ile Lys Glu Ser Asp Ile 355 360 365			1104
gaa att ata tta ccc gat ggt att tta tct ggt gta aat att ata ttt Glu Ile Ile Leu Pro Asp Gly Ile Leu Ser Gly Val Asn Ile Ile Phe 370 375 380			1152
act ggt gtt aac aaa gaa agt gaa att aaa aga ata tta tac ttt ttt Thr Gly Val Asn Lys Glu Ser Glu Ile Lys Arg Ile Leu Tyr Phe Phe 385 390 395 400			1200
aaa tca ttt gga tat aaa aat att aat aaa aca ata att gat aaa tta Lys Ser Phe Gly Tyr Lys Asn Ile Asn Lys Thr Ile Ile Asp Lys Leu 405 410 415			1248
tat atg tta gga tat gta aat ata tta aaa tat tta gaa aaa gat att Tyr Met Leu Gly Tyr Val Asn Ile Leu Lys Tyr Leu Glu Lys Asp Ile 420 425 430			1296
aat ata gaa gaa tat aat aat aaa aaa act tat att aaa tta ttg gaa Asn Ile Glu Glu Tyr Asn Asn Lys Lys Thr Tyr Ile Lys Leu Leu Glu 435 440 445			1344
gta att aaa gat ata aaa agt aaa aat tat aat atc gta gac ata tta Val Ile Lys Asp Ile Lys Ser Lys Asn Tyr Asn Ile Val Asp Ile Leu 450 455 460			1392
aca gca tta tct cta gat agt ata tca aaa tca aga gtt tgt gct att Thr Ala Leu Ser Leu Asp Ser Ile Ser Lys Ser Arg Val Cys Ala Ile 465 470 475 480			1440
tat aat gag ttt cca gat ttt ttg aaa gat aaa aat gaa aaa gat tat Tyr Asn Glu Phe Pro Asp Phe Leu Lys Asp Lys Asn Glu Lys Asp Tyr 485 490 495			1488

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agt tca ata aac ggt att gga aaa tct ata tca aaa aaa att aat gat      1536
Ser Ser Ile Asn Gly Ile Gly Lys Ser Ile Ser Lys Lys Ile Asn Asp
          500                      505                      510

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aat att ata aat aat tac gaa tat ata ata aat att tta aac gct tta      1584
Asn Ile Ile Asn Asn Tyr Glu Tyr Ile Ile Asn Ile Leu Asn Ala Leu
          515                      520                      525

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aat ata aag tat taa
Asn Ile Lys Tyr
          530

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<210> 59

<211> 687

<212> DNA

<213> Amsacta moorei entomopoxvirus

<220>

<221> exon

<222> (1) .. (687)

<223>

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<400> 59
atg agc gat aat ata aaa tgt aaa tat tgt aat tct ttt aac ata ata      48
Met Ser Asp Asn Ile Lys Cys Lys Tyr Cys Asn Ser Phe Asn Ile Ile
1          5          10          15

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```

aaa aat aaa gat ata tat tca tgt tgt gat tgc tca aat tgt tat aca      96
Lys Asn Lys Asp Ile Tyr Ser Cys Cys Asp Cys Ser Asn Cys Tyr Thr
          20          25          30

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aca tcg tca aaa aga ata aca aca ata agt agt gct tca aac aat aaa      144
Thr Ser Ser Lys Arg Ile Thr Thr Ile Ser Ser Ala Ser Asn Asn Lys
          35          40          45

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act ata cat tgt aat aat gtt tta aaa gaa ata tca aat acc agt att      192
Thr Ile His Cys Asn Asn Val Leu Lys Glu Ile Ser Asn Thr Ser Ile
          50          55          60

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tca tat gat ata gta gat ggt ttt cta aaa cta atc aat gat aat aat      240
Ser Tyr Asp Ile Val Asp Gly Phe Leu Lys Leu Ile Asn Asp Asn Asn
65          70          75          80

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```

tta aat aca aaa agt ata aca act gcg tta ggt tct gaa tat tta aaa      288
Leu Asn Thr Lys Ser Ile Thr Thr Ala Leu Gly Ser Glu Tyr Leu Lys

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85										90					95					
tca	aaa	ggt	ata	aaa	aat	tat	aga	act	acg	cat	aaa	tta	att	aat	atg	336				
Ser	Lys	Gly	Ile	Lys	Asn	Tyr	Arg	Thr	Thr	His	Lys	Leu	Ile	Asn	Met					
100										105					110					
tct	cta	tcg	gat	ggt	aat	aat	tgt	ata	tta	act	aaa	gac	gat	atc	ttt	384				
Ser	Leu	Ser	Asp	Gly	Asn	Asn	Cys	Ile	Leu	Thr	Lys	Asp	Asp	Ile	Phe					
115										120					125					
aga	att	aat	ata	att	ttt	gag	gat	ttt	aca	caa	ttt	ata	tat	aaa	aat	432				
Arg	Ile	Asn	Ile	Ile	Phe	Glu	Asp	Phe	Thr	Gln	Phe	Ile	Tyr	Lys	Asn					
130										135					140					
aat	tat	aca	aaa	act	ata	tct	tac	gaa	ttc	tgt	tta	gat	aga	ata	ttt	480				
Asn	Tyr	Thr	Lys	Thr	Ile	Ser	Tyr	Glu	Phe	Cys	Leu	Asp	Arg	Ile	Phe					
145										150					155					160
gat	att	ctt	aat	ata	aat	tat	gta	ata	aat	ttc	aat	tat	agc	aaa	cta	528				
Asp	Ile	Leu	Asn	Ile	Asn	Tyr	Val	Ile	Asn	Phe	Asn	Tyr	Ser	Lys	Leu					
165										170					175					
aat	aaa	aga	gac	gat	aaa	cca	gaa	ata	tgg	aat	aaa	tat	ata	att	gaa	576				
Asn	Lys	Arg	Asp	Asp	Lys	Pro	Glu	Ile	Trp	Asn	Lys	Tyr	Ile	Ile	Glu					
180										185					190					
tta	tat	aat	aaa	tca	ttg	att	aaa	tct	aat	aat	aaa	ttt	ata	ttt	aga	624				
Leu	Tyr	Asn	Lys	Ser	Leu	Ile	Lys	Ser	Asn	Asn	Lys	Phe	Ile	Phe	Arg					
195										200					205					
cca	aat	aat	att	att	ttt	aat	gaa	tat	ata	aaa	aat	aat	ata	tgt	ttg	672				
Pro	Asn	Asn	Ile	Ile	Phe	Asn	Glu	Tyr	Ile	Lys	Asn	Asn	Ile	Cys	Leu					
210										215					220					
cgt	aat	att	att	taa												687				
Arg	Asn	Ile	Ile																	
225																				

&lt;210&gt; 60

&lt;211&gt; 3906

&lt;212&gt; DNA

&lt;213&gt; Amsacta moorei entomopoxvirus

&lt;220&gt;

&lt;221&gt; exon

&lt;222&gt; (1) .. (3906)

&lt;223&gt;

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<400> 60
atg aca act ttt aaa tat act ttg tta gat aat agc aca ata gat gct      48
Met Thr Thr Phe Lys Tyr Thr Leu Leu Asp Asn Ser Thr Ile Asp Ala
1          5          10          15

att cca ata gtt att gat tct att gga aat gat aac gaa aat agt gta      96
Ile Pro Ile Val Ile Asp Ser Ile Gly Asn Asp Asn Glu Asn Ser Val
          20          25          30

aaa agt cct aaa tta ggc gga act aaa ttc aat gtg tgt tcg aca tgc      144
Lys Ser Pro Lys Leu Gly Gly Thr Lys Phe Asn Val Cys Ser Thr Cys
          35          40          45

aat tta aca aga gaa aat ggc gac atg ggt cat cca gga aga act cct      192
Asn Leu Thr Arg Glu Asn Gly Asp Met Gly His Pro Gly Arg Thr Pro
          50          55          60

tta aga gat atg tgt att gta aaa tct ggt tgt att aaa aat gtt ttg      240
Leu Arg Asp Met Cys Ile Val Lys Ser Gly Cys Ile Lys Asn Val Leu
65          70          75          80

gat aca cta aat aca tta aaa tta tgt aat agt tgt ttt atg ata aaa      288
Asp Thr Leu Asn Thr Leu Lys Leu Cys Asn Ser Cys Phe Met Ile Lys
          85          90          95

aat aat aca ata ttt tca gaa ata att gaa aaa tat aat agc gaa tat      336
Asn Asn Thr Ile Phe Ser Glu Ile Ile Glu Lys Tyr Asn Ser Glu Tyr
          100          105          110

aat att aat tta aaa aaa gaa ata tta tca tta tta aaa aac aat cgc      384
Asn Ile Asn Leu Lys Lys Glu Ile Leu Ser Leu Leu Lys Asn Asn Arg
          115          120          125

caa ggt ggg gta aaa tgt aat aat gaa aat tgt caa aat ata aca gga      432
Gln Gly Gly Val Lys Cys Asn Asn Glu Asn Cys Gln Asn Ile Thr Gly
          130          135          140

aca tat aaa tat aat caa aaa aaa tca tat ttt tac gta aaa aaa caa      480
Thr Tyr Lys Tyr Asn Gln Lys Lys Ser Tyr Phe Tyr Val Lys Lys Gln
145          150          155          160

aaa gat gaa atc att ctt aat aaa aca gtt tat act atg tta ctt gga      528
Lys Asp Glu Ile Ile Leu Asn Lys Thr Val Tyr Thr Met Leu Leu Gly
          165          170          175

att cct gat ata att tat aaa tgt gtt act gta cca tac gca gat tct      576
Ile Pro Asp Ile Ile Tyr Lys Cys Val Thr Val Pro Tyr Ala Asp Ser
          180          185          190

caa tta caa cct tat aaa gca ttt tac gct aat aat att ata att cct      624
Gln Leu Gln Pro Tyr Lys Ala Phe Tyr Ala Asn Asn Ile Ile Ile Pro
          195          200          205

gta tta cca tct aga cct cca aat tat ttt gat aat aaa gaa tct cat      672
Val Leu Pro Ser Arg Pro Pro Asn Tyr Phe Asp Asn Lys Glu Ser His

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210	215	220	
gtt atg aca aca aaa ttg ggt caa tta gtt ggc aca tca caa aaa tct Val Met Thr Thr Lys Leu Gly Gln Leu Val Gly Thr Ser Gln Lys Ser 225 230 235 240			720
aga gat gaa agt gaa gtt caa aaa ata tat aat gat att gat aat gtt Arg Asp Glu Ser Glu Val Gln Lys Ile Tyr Asn Asp Ile Asp Asn Val 245 250 255			768
aaa cca aat tct cca tat aaa act agt aac atg tta gtt acg tta aat Lys Pro Asn Ser Pro Tyr Lys Thr Ser Asn Met Leu Val Thr Leu Asn 260 265 270			816
ata caa gtt ggt ggt aac aaa aaa gga agt ata gtt aga tct aat ata Ile Gln Val Gly Gly Asn Lys Lys Gly Ser Ile Val Arg Ser Asn Ile 275 280 285			864
atg gct aga aga gcc gat aac aca gct aga tgt gta gct ggt cca act Met Ala Arg Arg Ala Asp Asn Thr Ala Arg Cys Val Ala Gly Pro Thr 290 295 300			912
atg gac aaa ata gga tat ata tat ata cca aaa ata gtg gct aag aca Met Asp Lys Ile Gly Tyr Ile Tyr Ile Pro Lys Ile Val Ala Lys Thr 305 310 315 320			960
tta aca tca tca ata tat tat aat aga ttt act gaa aat atg att aaa Leu Thr Ser Ser Ile Tyr Tyr Asn Arg Phe Thr Glu Asn Met Ile Lys 325 330 335			1008
gat atg tta gtt aat gat aat aac aaa att aaa tat ata tta tta tat Asp Met Leu Val Asn Asp Asn Asn Lys Ile Lys Tyr Ile Leu Leu Tyr 340 345 350			1056
aga tat gat caa tta aaa ccc aca aca tta tta aaa ata aaa cca caa Arg Tyr Asp Gln Leu Lys Pro Thr Thr Leu Leu Lys Ile Lys Pro Gln 355 360 365			1104
tct aga ctc aat aat tta tta aaa atg aaa tat gga gat aga ata gaa Ser Arg Leu Asn Asn Leu Leu Lys Met Lys Tyr Gly Asp Arg Ile Glu 370 375 380			1152
gtt gaa tta gaa gat aat gat gta ata tta ttt agt aga caa cca tct Val Glu Leu Glu Asp Asn Asp Val Ile Leu Phe Ser Arg Gln Pro Ser 385 390 395 400			1200
tta cat aaa ttt aat att cag gca ggt ata tgt aaa ata tgg gat aat Leu His Lys Phe Asn Ile Gln Ala Gly Ile Cys Lys Ile Trp Asp Asn 405 410 415			1248
aat aca ata gca aca cct acg ccg ata gca aat tct atg aat tta gat Asn Thr Ile Ala Thr Pro Thr Pro Ile Ala Asn Ser Met Asn Leu Asp 420 425 430			1296
tat gat ggt gat gaa atg aat gta tat aaa tta aaa tca tct gtg tca Tyr Asp Gly Asp Glu Met Asn Val Tyr Lys Leu Lys Ser Ser Val Ser 435 440 445			1344

gta gaa tca tta ttt act atg tta tct gtt aat atg att aaa aat aat	1392
Val Glu Ser Leu Phe Thr Met Leu Ser Val Asn Met Ile Lys Asn Asn	
450 455 460	
tat aat ttt tcg cca ata ttt ggg tta att caa gat caa ata ata tca	1440
Tyr Asn Phe Ser Pro Ile Phe Gly Leu Ile Gln Asp Gln Ile Ile Ser	
465 470 475 480	
gta cat atg ata tat aat att aaa gaa ttt tct cta caa gat gtt att	1488
Val His Met Ile Tyr Asn Ile Lys Glu Phe Ser Leu Gln Asp Val Ile	
485 490 495	
tat att tta gga gaa tat agt tat tat ata aga gat ata aat aaa aaa	1536
Tyr Ile Leu Gly Glu Tyr Ser Tyr Tyr Ile Arg Asp Ile Asn Lys Lys	
500 505 510	
aca tat tct gga aaa gaa tta tta tca tta tta ttt cca gat aat ctt	1584
Thr Tyr Ser Gly Lys Glu Leu Leu Ser Leu Leu Phe Pro Asp Asn Leu	
515 520 525	
aca tat gaa ggt atg ttt gat aat ggt aaa att aca tta tct aat ata	1632
Thr Tyr Glu Gly Met Phe Asp Asn Gly Lys Ile Thr Leu Ser Asn Ile	
530 535 540	
tca tct aaa caa gtt gta gct cag tca tat gaa tca ttt tca aat att	1680
Ser Ser Lys Gln Val Val Ala Gln Ser Tyr Glu Ser Phe Ser Asn Ile	
545 550 555 560	
cta tct caa tta aaa aat aat att tat gct gtg tat ttt ata gat gta	1728
Leu Ser Gln Leu Lys Asn Asn Ile Tyr Ala Val Tyr Phe Ile Asp Val	
565 570 575	
ata tta tat gta gct aga aat ttt ata aat ttg tat agt ttt agc gtt	1776
Ile Leu Tyr Val Ala Arg Asn Phe Ile Asn Leu Tyr Ser Phe Ser Val	
580 585 590	
tcg tta aaa gat att att cca gat ata tat ttt att gac gat gtt caa	1824
Ser Leu Lys Asp Ile Ile Pro Asp Ile Tyr Phe Ile Asp Asp Val Gln	
595 600 605	
gaa tac att aat aat tgt tgt aaa gtt ata caa tat gtt gcg cta caa	1872
Glu Tyr Ile Asn Asn Cys Cys Lys Val Ile Gln Tyr Val Ala Leu Gln	
610 615 620	
tat tat att aaa aaa gat cat ata ata aaa tta act tat gat gaa atg	1920
Tyr Tyr Ile Lys Lys Asp His Ile Ile Lys Leu Thr Tyr Asp Glu Met	
625 630 635 640	
gaa aat ata aga ata caa aac ggt aat aat ata ata tct aat gtt aaa	1968
Glu Asn Ile Arg Ile Gln Asn Gly Asn Asn Ile Ile Ser Asn Val Lys	
645 650 655	
aat aaa ata aat aat cta ttt aaa gat gag aaa tta aat act ata atg	2016
Asn Lys Ile Asn Asn Leu Phe Lys Asp Glu Lys Leu Asn Thr Ile Met	
660 665 670	

atg atg aaa aat tca ggc tat aaa ata aca tta gat gaa tta gta aca	2064
Met Met Lys Asn Ser Gly Tyr Lys Ile Thr Leu Asp Glu Leu Val Thr	
675 680 685	
gtg ttg ggt tgt act gga caa caa gga att gat tca gat gat ata ccg	2112
Val Leu Gly Cys Thr Gly Gln Gln Gly Ile Asp Ser Asp Asp Ile Pro	
690 695 700	
aaa ccc gga att atg gga aga gta ttt gat tca aca tta cct gga agt	2160
Lys Pro Gly Ile Met Gly Arg Val Phe Asp Ser Thr Leu Pro Gly Ser	
705 710 715 720	
tta gac ata gaa tca tta gga tat gta aaa tca tca act ata aaa ggt	2208
Leu Asp Ile Glu Ser Leu Gly Tyr Val Lys Ser Ser Thr Ile Lys Gly	
725 730 735	
tta aaa ttc gaa gaa ttg gca ttt cat aca aaa tac aat tca att aaa	2256
Leu Lys Phe Glu Glu Leu Ala Phe His Thr Lys Tyr Asn Ser Ile Lys	
740 745 750	
aaa ata tta aaa ata aca tgc gag aca tca tcg gca ggt agt att ggt	2304
Lys Ile Leu Lys Ile Thr Cys Glu Thr Ser Ser Ala Gly Ser Ile Gly	
755 760 765	
aga aaa tta gtt aaa ttt atg gaa ggt gtt aaa gta gat cat ttg ggt	2352
Arg Lys Leu Val Lys Phe Met Glu Gly Val Lys Val Asp His Leu Gly	
770 775 780	
aga tcc gta tta aat aat gat att ata tgg tat aat aca aat cat att	2400
Arg Ser Val Leu Asn Asn Asp Ile Ile Trp Tyr Asn Thr Asn His Ile	
785 790 795 800	
aaa atg aca ggt ggt gat ata tct aaa gta gaa ata tta act cct agt	2448
Lys Met Thr Gly Gly Asp Ile Ser Lys Val Glu Ile Leu Thr Pro Ser	
805 810 815	
tta gaa atg gta aat tac aca ctt ata aaa gaa ata tat aac gaa aat	2496
Leu Glu Met Val Asn Tyr Thr Leu Ile Lys Glu Ile Tyr Asn Glu Asn	
820 825 830	
aaa aaa tat tta tta act aat ttt aat act gaa ata aat aaa gaa ttt	2544
Lys Lys Tyr Leu Leu Thr Asn Phe Asn Thr Glu Ile Asn Lys Glu Phe	
835 840 845	
att ttt cca att aat ata aaa tta gag att caa tca ttt tat aat aaa	2592
Ile Phe Pro Ile Asn Ile Lys Leu Glu Ile Gln Ser Phe Tyr Asn Lys	
850 855 860	
aaa tca act cct ata tct gat ata gat gca tta aaa tta att gat gaa	2640
Lys Ser Thr Pro Ile Ser Asp Ile Asp Ala Leu Lys Leu Ile Asp Glu	
865 870 875 880	
ttt ata gaa tat gtc tat att aat ata tat ttt tac aac att aca ata	2688
Phe Ile Glu Tyr Val Tyr Ile Asn Ile Tyr Phe Tyr Asn Ile Thr Ile	
885 890 895	
gat tgg ttt aaa tat att tta tat aca tat cta gat aga aat aca gta	2736

Asp	Trp	Phe	Lys	Tyr	Ile	Leu	Tyr	Thr	Tyr	Leu	Asp	Arg	Asn	Thr	Val		
			900					905					910				
gaa	aaa	tat	aat	aaa	aaa	tat	tct	aaa	gaa	tta	tta	aat	tat	ata	ata	2784	
Glu	Lys	Tyr	Asn	Lys	Lys	Tyr	Ser	Lys	Glu	Leu	Leu	Asn	Tyr	Ile	Ile		
		915					920					925					
aat	aaa	att	aaa	tta	aaa	tta	cta	aat	tca	tta	aat	cca	ggt	tat	cct	2832	
Asn	Lys	Ile	Lys	Leu	Lys	Leu	Leu	Asn	Ser	Leu	Asn	Pro	Gly	Tyr	Pro		
		930				935					940						
att	gga	tta	gaa	tac	gca	aat	aat	att	caa	gaa	aaa	ttt	aca	caa	caa	2880	
Ile	Gly	Leu	Glu	Tyr	Ala	Asn	Asn	Ile	Gln	Glu	Lys	Phe	Thr	Gln	Gln		
		945			950					955					960		
tca	tta	tcg	tct	ttt	cac	act	act	aaa	aaa	tca	gga	aca	gca	tca	acc	2928	
Ser	Leu	Ser	Ser	Phe	His	Thr	Thr	Lys	Lys	Ser	Gly	Thr	Ala	Ser	Thr		
				965				970					975				
caa	tta	gga	ttt	tcg	gat	ttt	aaa	gat	act	gta	gaa	ttg	agt	aaa	aaa	2976	
Gln	Leu	Gly	Phe	Ser	Asp	Phe	Lys	Asp	Thr	Val	Glu	Leu	Ser	Lys	Lys		
			980				985					990					
aat	aaa	aga	gat	att	gta	att	gct	ttt	aca	aca	cac	aga	tat	aaa	tta	3024	
Asn	Lys	Arg	Asp	Ile	Val	Ile	Ala	Phe	Thr	Thr	His	Arg	Tyr	Lys	Leu		
		995					1000					1005					
gaa	gat	att	aag	aag	caa	atg	gaa	tac	ttg	tgt	tta	aag	aat	ttt		3069	
Glu	Asp	Ile	Lys	Lys	Gln	Met	Glu	Tyr	Leu	Cys	Leu	Lys	Asn	Phe			
		1010				1015					1020						
aat	cca	aaa	ata	aat	atc	ata	gaa	gaa	act	gaa	tct	gat	atg	gta		3114	
Asn	Pro	Lys	Ile	Asn	Ile	Ile	Glu	Glu	Thr	Glu	Ser	Asp	Met	Val			
		1025				1030					1035						
ata	agt	gta	agt	ata	aaa	aaa	tac	tat	att	aat	gac	aaa	ata	tct		3159	
Ile	Ser	Val	Ser	Ile	Lys	Lys	Tyr	Tyr	Ile	Asn	Asp	Lys	Ile	Ser			
		1040				1045					1050						
tta	tat	cat	tac	tta	caa	atg	tat	ata	gaa	tat	tta	gaa	aat	aat		3204	
Leu	Tyr	His	Tyr	Leu	Gln	Met	Tyr	Ile	Glu	Tyr	Leu	Glu	Asn	Asn			
		1055				1060					1065						
aaa	att	att	aaa	ggc	tat	tgg	ata	act	atg	aaa	tta	aaa	gat	aat		3249	
Lys	Ile	Ile	Lys	Gly	Tyr	Trp	Ile	Thr	Met	Lys	Leu	Lys	Asp	Asn			
		1070				1075					1080						
gat	ata	aca	gtg	ata	ttt	gga	gtt	aaa	att	aaa	act	cct	tat	aat		3294	
Asp	Ile	Thr	Val	Ile	Phe	Gly	Val	Lys	Ile	Lys	Thr	Pro	Tyr	Asn			
		1085				1090					1095						
ata	aat	aaa	ata	tat	atg	ata	aaa	agt	ata	cca	gtt	tcg	gtt	tct		3339	
Ile	Asn	Lys	Ile	Tyr	Met	Ile	Lys	Ser	Ile	Pro	Val	Ser	Val	Ser			
		1100				1105					1110						
aaa	ggt	aaa	ata	agt	aac	ata	aat	tta	gag	ata	gaa	gat	gtt	aaa		3384	
Lys	Gly	Lys	Ile	Ser	Asn	Ile	Asn	Leu	Glu	Ile	Glu	Asp	Val	Lys			



1115	1120	1125	
atg tat aat aat aat ttg gaa gaa caa aat ggt tat aga tta aaa			3429
Met Tyr Asn Asn Asn Leu Glu Glu Gln Asn Gly Tyr Arg Leu Lys			
1130	1135	1140	
ttc tat att gat agt gtc aca gat ttt att aat ttt gat acg aga			3474
Phe Tyr Ile Asp Ser Val Thr Asp Phe Ile Asn Phe Asp Thr Arg			
1145	1150	1155	
gat gtt tat ctg gaa tta ggt ccg tgg ttt acg tat aat tcg ttt			3519
Asp Val Tyr Leu Glu Leu Gly Pro Trp Phe Thr Tyr Asn Ser Phe			
1160	1165	1170	
ggc ata caa ttt gct gaa tat tct att aga cgt aga tta gtt tcg			3564
Gly Ile Gln Phe Ala Glu Tyr Ser Ile Arg Arg Arg Leu Val Ser			
1175	1180	1185	
tct aca aaa gaa aaa agt atg gaa ata tgt tat ata ata tta tcg			3609
Ser Thr Lys Glu Lys Ser Met Glu Ile Cys Tyr Ile Ile Leu Ser			
1190	1195	1200	
aaa ttg atg tgt tta tct tcc gaa atg tat aat ata aaa aga ata			3654
Lys Leu Met Cys Leu Ser Ser Glu Met Tyr Asn Ile Lys Arg Ile			
1205	1210	1215	
aga gag ggt aaa caa aat gtt ata aaa tca gca ata cat ggt agt			3699
Arg Glu Gly Lys Gln Asn Val Ile Lys Ser Ala Ile His Gly Ser			
1220	1225	1230	
tcg gat gct ata aca aca gct gca tat aat aat ata ata gat cca			3744
Ser Asp Ala Ile Thr Thr Ala Ala Tyr Asn Asn Ile Ile Asp Pro			
1235	1240	1245	
aac aat gat ata tat tct caa ata tta tca agt caa att atg aaa			3789
Asn Asn Asp Ile Tyr Ser Gln Ile Leu Ser Ser Gln Ile Met Lys			
1250	1255	1260	
tta gga cat gga tat tat gat tgt tat tta aat tta aat aga tat			3834
Leu Gly His Gly Tyr Tyr Asp Cys Tyr Leu Asn Leu Asn Arg Tyr			
1265	1270	1275	
gat tct att aac ata aat tct gtc acc gaa caa gat ata aat ata			3879
Asp Ser Ile Asn Ile Asn Ser Val Thr Glu Gln Asp Ile Asn Ile			
1280	1285	1290	
aca agt gaa ata att gaa aat ttc taa			3906
Thr Ser Glu Ile Ile Glu Asn Phe			
1295	1300		

&lt;210&gt; 61

&lt;211&gt; 483

&lt;212&gt; DNA

<213> Amsacta moorei entomopoxvirus

<220>

<221> exon

<222> (1) .. (483)

<223>

<400> 61

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Met Glu Arg Ser Leu Gln Ile Ile Asn Asn Thr Thr Ser Thr Leu Ser	
1 5 10 15	
aga ata aca tca cca atc gat aat att aga tat att ttt gat ctt att	96
Arg Ile Thr Ser Pro Ile Asp Asn Ile Arg Tyr Ile Phe Asp Leu Ile	
20 25 30	
aac aca agt ggt aat ggt gaa att acg gca gaa gaa tta cta aat ttt	144
Asn Thr Ser Gly Asn Gly Glu Ile Thr Ala Glu Glu Leu Leu Asn Phe	
35 40 45	
tta att gtt att gat cca act ata aat tta tct gat gtt cgt gcg tta	192
Leu Ile Val Ile Asp Pro Thr Ile Asn Leu Ser Asp Val Arg Ala Leu	
50 55 60	
att gcc aca tat gat ttg aat aat aac aat acg tta agt ttt gat gaa	240
Ile Ala Thr Tyr Asp Leu Asn Asn Asn Asn Thr Leu Ser Phe Asp Glu	
65 70 75 80	
ttt gtt cca ata ata ggt att aat ata act gat gaa aaa tta aga gaa	288
Phe Val Pro Ile Ile Gly Ile Asn Ile Thr Asp Glu Lys Leu Arg Glu	
85 90 95	
gca ttt gat tct ata aca act gat ggt gat gtc gat ctt gat aaa ttt	336
Ala Phe Asp Ser Ile Thr Thr Asp Gly Asp Val Asp Leu Asp Lys Phe	
100 105 110	
aga aca tat tat aat tta tta caa att act ccc ata tat aga cat act	384
Arg Thr Tyr Tyr Asn Leu Leu Gln Ile Thr Pro Ile Tyr Arg His Thr	
115 120 125	
aac gat caa tat ata gat ata ata att aga atg atc gga agt agt caa	432
Asn Asp Gln Tyr Ile Asp Ile Ile Ile Arg Met Ile Gly Ser Ser Gln	
130 135 140	
gaa gaa ttt ata gca ttt tgg aat tac ata aat act caa gta aat gga	480
Glu Glu Phe Ile Ala Phe Trp Asn Tyr Ile Asn Thr Gln Val Asn Gly	
145 150 155 160	
taa	483

&lt;210&gt; 62

&lt;211&gt; 540

&lt;212&gt; DNA

&lt;213&gt; Amsacta moorei entomopoxvirus

&lt;220&gt;

&lt;221&gt; exon

&lt;222&gt; (1) .. (540)

&lt;223&gt;

&lt;400&gt; 62

atg gac aat aat aca att act aaa cat att ggc tat aat act tta caa	48
Met Asp Asn Asn Thr Ile Thr Lys His Ile Gly Tyr Asn Thr Leu Gln	
1 5 10 15	

gtt gtt aca gaa att tct att caa tta gaa agc aaa caa ata aat aat	96
Val Val Thr Glu Ile Ser Ile Gln Leu Glu Ser Lys Gln Ile Asn Asn	
20 25 30	

aat att aga caa gaa att gta tca aat ata aaa aat aat ata ata aat	144
Asn Ile Arg Gln Glu Ile Val Ser Asn Ile Lys Asn Asn Ile Ile Asn	
35 40 45	

aaa act agc ggt gtt aat tat att tta tca gtt gat tat caa tca ata	192
Lys Thr Ser Gly Val Asn Tyr Ile Leu Ser Val Asp Tyr Gln Ser Ile	
50 55 60	

tta aat aat gaa tta cca tta tta aga tta aat aat gta tat aca caa	240
Leu Asn Asn Glu Leu Pro Leu Leu Arg Leu Asn Asn Val Tyr Thr Gln	
65 70 75 80	

gaa tta gtt gtt aaa tta ccc gta aca tat cta tat ttt aca aaa aat	288
Glu Leu Val Val Lys Leu Pro Val Thr Tyr Leu Tyr Phe Thr Lys Asn	
85 90 95	

caa ata ata aaa gct tat ttg aca att att gaa gga gat aat cca cat	336
Gln Ile Ile Lys Ala Tyr Leu Thr Ile Ile Glu Gly Asp Asn Pro His	
100 105 110	

gta gtt gca tat aac aaa tat ata tat tgt aat ata att tta gat cat	384
Val Val Ala Tyr Asn Lys Tyr Ile Tyr Cys Asn Ile Ile Leu Asp His	
115 120 125	

aat ttc act ata aat atg tca gaa aaa tta tta ata ttt aag aac aaa	432
Asn Phe Thr Ile Asn Met Ser Glu Lys Leu Leu Ile Phe Lys Asn Lys	
130 135 140	

gaa tat aaa aat aga gat gaa tgt tat gta aaa ata atc gat ata tat 480  
 Glu Tyr Lys Asn Arg Asp Glu Cys Tyr Val Lys Ile Ile Asp Ile Tyr  
 145 150 155 160

agt tca gaa aaa aat aat aaa ata cca tgc aaa ggt att ttg caa gac 528  
 Ser Ser Glu Lys Asn Asn Lys Ile Pro Cys Lys Gly Ile Leu Gln Asp  
 165 170 175

gaa gaa ata taa 540  
 Glu Glu Ile

<210> 63

<211> 735

<212> DNA

<213> Amsacta moorei entomopoxvirus

<220>

<221> exon

<222> (1) .. (735)

<223>

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 Met Asn Asn Ile Ser Tyr Lys Asn Phe Ile Glu Asn Ile Pro Glu Lys  
 1 5 10 15

tgg tta gat gtg ata gat aaa aaa caa tta gaa tat gct cat cat aaa 96  
 Trp Leu Asp Val Ile Asp Lys Lys Gln Leu Glu Tyr Ala His His Lys  
 20 25 30

tta aaa aat gaa tct att att aaa cca tct ata aat aat ata ttt aaa 144  
 Leu Lys Asn Glu Ser Ile Ile Lys Pro Ser Ile Asn Asn Ile Phe Lys  
 35 40 45

tgt ttt aaa tat ttt aat ccc gat caa gtt aaa gta att att tta ggt 192  
 Cys Phe Lys Tyr Phe Asn Pro Asp Gln Val Lys Val Ile Ile Leu Gly  
 50 55 60

cag gat cct tat cct act gtt gga atg gct gat ggt tta gca ttt tcc 240  
 Gln Asp Pro Tyr Pro Thr Val Gly Met Ala Asp Gly Leu Ala Phe Ser  
 65 70 75 80

tgt tct aat aat agt aat tat att cct aaa tct tta caa aac ata ata 288  
 Cys Ser Asn Asn Ser Asn Tyr Ile Pro Lys Ser Leu Gln Asn Ile Ile

85	90	95	
aaa gaa ata tta aaa caa aat aaa aaa tat gat atg atg aaa aat att			336
Lys Glu Ile Leu Lys Gln Asn Lys Lys Tyr Asp Met Met Lys Asn Ile			
100	105	110	
aat atg aat tat att aat gta aat cta gaa ttt tta gcg aaa caa caa			384
Asn Met Asn Tyr Ile Asn Val Asn Leu Glu Phe Leu Ala Lys Gln Gln			
115	120	125	
att tta tta ttt aat acg ata ttg aca gtt ggt gat gag cca atg tca			432
Ile Leu Leu Phe Asn Thr Ile Leu Thr Val Gly Asp Glu Pro Met Ser			
130	135	140	
cac aaa cat att tgg gaa tca ttt tca aat tct att att aaa aaa tta			480
His Lys His Ile Trp Glu Ser Phe Ser Asn Ser Ile Ile Lys Lys Leu			
145	150	155	160
tca tta att aat aat aat ata gta ttt ata tta ttt ggt gca aaa gct			528
Ser Leu Ile Asn Asn Asn Ile Val Phe Ile Leu Phe Gly Ala Lys Ala			
165	170	175	
cat aat aaa att tat ttt atc gaa aat aaa aaa aat cat tgt att atc			576
His Asn Lys Ile Tyr Phe Ile Glu Asn Lys Lys Asn His Cys Ile Ile			
180	185	190	
aaa aca agt cat cct tct aat tta tct tgt tat aaa gat gga tat gat			624
Lys Thr Ser His Pro Ser Asn Leu Ser Cys Tyr Lys Asp Gly Tyr Asp			
195	200	205	
aaa tat gtt cct ttt aat aat tca gat tgt ttt aat att tgt aac gaa			672
Lys Tyr Val Pro Phe Asn Asn Ser Asp Cys Phe Asn Ile Cys Asn Glu			
210	215	220	
tat ctt ata aaa aat aat ata aaa ccg ata gat tgg tta tct gaa tta			720
Tyr Leu Ile Lys Asn Asn Ile Lys Pro Ile Asp Trp Leu Ser Glu Leu			
225	230	235	240
ata aaa aat aat taa			735
Ile Lys Asn Asn			

&lt;210&gt; 64

&lt;211&gt; 714

&lt;212&gt; DNA

&lt;213&gt; Amsacta moorei entomopoxvirus

&lt;220&gt;

&lt;221&gt; exon

&lt;222&gt; (1) .. (714)

&lt;223&gt;

&lt;400&gt; 64

atg gaa aat tat gat ttt aaa att gat aaa tat act cat ata gga aat	48
Met Glu Asn Tyr Asp Phe Lys Ile Asp Lys Tyr Thr His Ile Gly Asn	
1 5 10 15	
cgt agt tat aac gat gat tat ata ttt ata aaa aaa aat ata aat tat	96
Arg Ser Tyr Asn Asp Asp Tyr Ile Phe Ile Lys Lys Asn Ile Asn Tyr	
20 25 30	
atc atg ttt gta ata att gac gga cac gga ggt tca gaa tgt tct aaa	144
Ile Met Phe Val Ile Ile Asp Gly His Gly Gly Ser Glu Cys Ser Lys	
35 40 45	
ata ttt ata aaa tta ttt aat aaa aat ttt aat cca aaa cca tat gta	192
Ile Phe Ile Lys Leu Phe Asn Lys Asn Phe Asn Pro Lys Pro Tyr Val	
50 55 60	
gat att gga tta tat ata aaa aat tta ttt ata aaa att aat aaa aca	240
Asp Ile Gly Leu Tyr Ile Lys Asn Leu Phe Ile Lys Ile Asn Lys Thr	
65 70 75 80	
att tta aat aat aaa att aca tct gga gca tgt gta tct ggt att tat	288
Ile Leu Asn Asn Lys Ile Thr Ser Gly Ala Cys Val Ser Gly Ile Tyr	
85 90 95	
att gat aat aat aaa aca ata ata ttt caa tta gga gat aca aaa ata	336
Ile Asp Asn Asn Lys Thr Ile Ile Phe Gln Leu Gly Asp Thr Lys Ile	
100 105 110	
tat tta tat aat aac aat aaa tta aca tat gaa aca ata caa cat gat	384
Tyr Leu Tyr Asn Asn Asn Lys Leu Thr Tyr Glu Thr Ile Gln His Asp	
115 120 125	
ata tca aat aaa tac gaa aga aat aaa ttt ttt aaa gat ttt att tat	432
Ile Ser Asn Lys Tyr Glu Arg Asn Lys Phe Phe Lys Asp Phe Ile Tyr	
130 135 140	
tca gat att cca aga tta ttt gga aag tta aca gtt aca agg gca ata	480
Ser Asp Ile Pro Arg Leu Phe Gly Lys Leu Thr Val Thr Arg Ala Ile	
145 150 155 160	
gga aat ttt gat tta aat ata aaa tat ata cct aaa ata gat tat att	528
Gly Asn Phe Asp Leu Asn Ile Lys Tyr Ile Pro Lys Ile Asp Tyr Ile	
165 170 175	
tct aat aat agt tat aat aaa att att tta tgc aca gat gga gtg tat	576
Ser Asn Asn Ser Tyr Asn Lys Ile Ile Leu Cys Thr Asp Gly Val Tyr	
180 185 190	
aaa aaa ata aat ata aat atc gat gat act gct aaa gaa aat att aat	624
Lys Lys Ile Asn Ile Asn Ile Asp Asp Thr Ala Lys Glu Asn Ile Asn	

195	200	205	
aaa tgt tta aaa aat cct cct aat gat aat atg act atg atg att ata			672
Lys Cys Leu Lys Asn Pro Pro Asn Asp Asn Met Thr Met Met Ile Ile			
210	215	220	
aat tta tca aat ata tta cat tta ata aat aaa aac ata taa			714
Asn Leu Ser Asn Ile Leu His Leu Ile Asn Lys Asn Ile			
225	230	235	
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<222> (1) .. (474)			
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<400> 65			
atg tta cct tat aaa tgg aat aat tat ttt gca cac gga act ata ata			48
Met Leu Pro Tyr Lys Trp Asn Asn Tyr Phe Ala His Gly Thr Ile Ile			
1	5	10	15
aag tgt ata aat aca ata tgt ttc aaa ctt ccg tgc aat ggt act gaa			96
Lys Cys Ile Asn Thr Ile Cys Phe Lys Leu Pro Cys Asn Gly Thr Glu			
20	25	30	
tgg gat ata tgt aaa tta ata aat act ttt cct aat tta aaa att gta			144
Trp Asp Ile Cys Lys Leu Ile Asn Thr Phe Pro Asn Leu Lys Ile Val			
35	40	45	
ata gat ttt aga tat tca gaa aca tgt tat aat cca tct gat ctt aat			192
Ile Asp Phe Arg Tyr Ser Glu Thr Cys Tyr Asn Pro Ser Asp Leu Asn			
50	55	60	
aaa tta ggt ata gaa tat ata aaa ata cca ata aaa gca caa tct tta			240
Lys Leu Gly Ile Glu Tyr Ile Lys Ile Pro Ile Lys Ala Gln Ser Leu			
65	70	75	80
cca aca gat gat aaa ata aat aaa ttt ttt aat att att gat aaa tat			288
Pro Thr Asp Asp Lys Ile Asn Lys Phe Phe Asn Ile Ile Asp Lys Tyr			
85	90	95	
att gaa tta aaa tat tta ata gga ata cat tgt act cat ggc att aat			336

Ile	Glu	Leu	Lys	Tyr	Leu	Ile	Gly	Ile	His	Cys	Thr	His	Gly	Ile	Asn	
			100					105					110			
aga	act	gga	tat	atg	gtt	tgt	aaa	tac	tta	ata	tat	aaa	ttt	aaa	att	384
Arg	Thr	Gly	Tyr	Met	Val	Cys	Lys	Tyr	Leu	Ile	Tyr	Lys	Phe	Lys	Ile	
		115					120					125				
cca	cct	tat	gtt	gct	ata	aat	att	ttc	gaa	aaa	aat	aga	gga	tat	tat	432
Pro	Pro	Tyr	Val	Ala	Ile	Asn	Ile	Phe	Glu	Lys	Asn	Arg	Gly	Tyr	Tyr	
		130				135					140					
ata	gaa	aga	gaa	ata	tat	ata	aat	aat	tta	tta	tat	ttt	taa			474
Ile	Glu	Arg	Glu	Ile	Tyr	Ile	Asn	Asn	Leu	Leu	Tyr	Phe				
145					150				155							

&lt;210&gt; 66

&lt;211&gt; 870

&lt;212&gt; DNA

&lt;213&gt; Amsacta moorei entomopoxvirus

&lt;220&gt;

&lt;221&gt; exon

&lt;222&gt; (1) .. (870)

&lt;223&gt;

<400>	66															
atg	gaa	aat	tat	cat	att	att	ata	tta	aca	att	aaa	aga	aat	tct	gac	48
Met	Glu	Asn	Tyr	His	Ile	Ile	Ile	Leu	Thr	Ile	Lys	Arg	Asn	Ser	Asp	
1				5				10					15			
aga	tta	caa	aaa	cta	gaa	aat	ata	tta	tct	tgt	caa	aat	tta	tta	tat	96
Arg	Leu	Gln	Lys	Leu	Glu	Asn	Ile	Leu	Ser	Cys	Gln	Asn	Leu	Leu	Tyr	
			20					25					30			
aat	aaa	gat	tat	agt	gta	ttt	tat	gga	ata	gat	tat	aaa	aat	ata	aat	144
Asn	Lys	Asp	Tyr	Ser	Val	Phe	Tyr	Gly	Ile	Asp	Tyr	Lys	Asn	Ile	Asn	
		35					40					45				
aaa	aat	aat	tta	aaa	aat	ata	tgt	aaa	aaa	gga	ttt	aaa	aac	aca	tgt	192
Lys	Asn	Asn	Leu	Lys	Asn	Ile	Cys	Lys	Lys	Gly	Phe	Lys	Asn	Thr	Cys	
		50				55					60					
cct	tat	tca	act	tta	gca	tgt	gcg	tca	tca	cat	att	cta	tta	tggt	aaa	240
Pro	Tyr	Ser	Thr	Leu	Ala	Cys	Ala	Ser	Ser	His	Ile	Leu	Leu	Trp	Lys	
65					70					75					80	



tat ata tca aaa tta aaa gat aaa tat aaa tat att ata ata tta gaa	288
Tyr Ile Ser Lys Leu Lys Asp Lys Tyr Lys Tyr Ile Ile Ile Leu Glu	
85 90 95	
gat gat aca tat ata aat gta tca gag tat aat aaa cat aca aat aca	336
Asp Asp Thr Tyr Ile Asn Val Ser Glu Tyr Asn Lys His Thr Asn Thr	
100 105 110	
gtt gaa gaa tta tta aaa aat aat agt ata gta ttt tta tat tct gat	384
Val Glu Glu Leu Leu Lys Asn Asn Ser Ile Val Phe Leu Tyr Ser Asp	
115 120 125	
tgt tat ata atg gga act acc atc aaa tca acc aac aat gat aca aaa	432
Cys Tyr Ile Met Gly Thr Thr Ile Lys Ser Thr Asn Asn Asp Thr Lys	
130 135 140	
ata aca tat aat cca aag ttt cac gtt tct atg ggt tgt tat tgt ata	480
Ile Thr Tyr Asn Pro Lys Phe His Val Ser Met Gly Cys Tyr Cys Ile	
145 150 155 160	
aca cca atc act gct act aaa tta tat tat ttc tat ata aaa tct aga	528
Thr Pro Ile Thr Ala Thr Lys Leu Tyr Tyr Phe Tyr Ile Lys Ser Arg	
165 170 175	
gta tgg ttc cac ata gat ttt caa tta aat ttt gat ata cat aat ata	576
Val Trp Phe His Ile Asp Phe Gln Leu Asn Phe Asp Ile His Asn Ile	
180 185 190	
tca tta aat aga tat att tat ata gct gct aat gta tgt aat caa tat	624
Ser Leu Asn Arg Tyr Ile Tyr Ile Ala Ala Asn Val Cys Asn Gln Tyr	
195 200 205	
gaa gga aat aaa tca tct atg ggt tta aaa cat aat aat ata atg tta	672
Glu Gly Asn Lys Ser Ser Met Gly Leu Lys His Asn Asn Ile Met Leu	
210 215 220	
ata cct ata gaa aat aca aaa tta atg aga ata ata tct act cct att	720
Ile Pro Ile Glu Asn Thr Lys Leu Met Arg Ile Ile Ser Thr Pro Ile	
225 230 235 240	
ata aga gtt aat gaa gct gaa ata gat ttt tat ata ata ata atg tta	768
Ile Arg Val Asn Glu Ala Glu Ile Asp Phe Tyr Ile Ile Ile Met Leu	
245 250 255	
atc tca ctt atc gct agt tta tat ttc ttt ggt ttt aat att tct gcc	816
Ile Ser Leu Ile Ala Ser Leu Tyr Phe Phe Gly Phe Asn Ile Ser Ala	
260 265 270	
tta ata ttt tta tta ttt ata gta gta gat gtt gcg gag aat gca aaa	864
Leu Ile Phe Leu Leu Phe Ile Val Val Asp Val Ala Glu Asn Ala Lys	
275 280 285	
aaa taa	870
Lys	

&lt;210&gt; 67

&lt;211&gt; 1830

&lt;212&gt; DNA

&lt;213&gt; Amsacta moorei entomopoxvirus

&lt;220&gt;

&lt;221&gt; exon

&lt;222&gt; (1)..(1830)

&lt;223&gt;

&lt;400&gt; 67

atg aat ata aaa tta tta aaa aat gga atg cga att att aat aat aat	48
Met Asn Ile Lys Leu Leu Lys Asn Gly Met Arg Ile Ile Asn Asn Asn	
1 5 10 15	
ttt gat aat aat aat tta ata aat ata tct ata aat aat ttt ggt caa	96
Phe Asp Asn Asn Asn Leu Ile Asn Ile Ser Ile Asn Asn Phe Gly Gln	
20 25 30	
aat tta tca ata tat tat aag aat tat aag tta ata cat ctc ata gaa	144
Asn Leu Ser Ile Tyr Tyr Lys Asn Tyr Lys Leu Ile His Leu Ile Glu	
35 40 45	
cat ata tta gta tca atg cta ata gta tat aca ggt gaa tta tca ttt	192
His Ile Leu Val Ser Met Leu Ile Val Tyr Thr Gly Glu Leu Ser Phe	
50 55 60	
tgg aac gga tat aca aat tca aat aat att aat ata tat tat aat aat	240
Trp Asn Gly Tyr Thr Asn Ser Asn Asn Ile Asn Ile Tyr Tyr Asn Asn	
65 70 75 80	
ata atg aat ata tca cat aat aaa ata att gat gcg ata ctt cgt tta	288
Ile Met Asn Ile Ser His Asn Lys Ile Ile Asp Ala Ile Leu Arg Leu	
85 90 95	
ttt aat aaa aat ggt att ttt gtt gat gaa aat ata ata aat tat aaa	336
Phe Asn Lys Asn Gly Ile Phe Val Asp Glu Asn Ile Ile Asn Tyr Lys	
100 105 110	
ttt tta gaa aat gaa aat aaa ata tta aat aat gaa aaa aat ttt aga	384
Phe Leu Glu Asn Glu Asn Lys Ile Leu Asn Asn Glu Lys Asn Phe Arg	
115 120 125	
tta tta aca gat aaa tat gaa ata aat cct ata tta tat ctt tta aca	432
Leu Leu Thr Asp Lys Tyr Glu Ile Asn Pro Ile Leu Tyr Leu Leu Thr	
130 135 140	

aat gat gtt tat tta gaa gaa aat aat caa aaa ata ata tct gat gtt	480
Asn Asp Val Tyr Leu Glu Glu Asn Asn Gln Lys Ile Ile Ser Asp Val	
145 150 155 160	
aaa ttt att aat gat gta ttg tcg gat att aat gtg tca gat att ata	528
Lys Phe Ile Asn Asp Val Leu Ser Asp Ile Asn Val Ser Asp Ile Ile	
165 170 175	
ttt tat act tca aat aca gat ttt ttt aat ata tta tat ccg cga tta	576
Phe Tyr Thr Ser Asn Thr Asp Phe Phe Asn Ile Leu Tyr Pro Arg Leu	
180 185 190	
gat aaa ata att ttt aat aaa act aaa aat aaa aat aaa ttt cta	624
Asp Lys Ile Ile Phe Asn Lys Thr Lys Asn Lys Lys Asn Lys Phe Leu	
195 200 205	
aca tta ccc att tat aaa tct agt ttt aaa aat agt ata tat tta ttt	672
Thr Leu Pro Ile Tyr Lys Ser Ser Phe Lys Asn Ser Ile Tyr Leu Phe	
210 215 220	
tct ttc gat caa aat aat aga tat tat agt ata act att aaa ttt aat	720
Ser Phe Asp Gln Asn Asn Arg Tyr Tyr Ser Ile Thr Ile Lys Phe Asn	
225 230 235 240	
tta tta aaa tat gtt ata att gga tat atg att gat aaa tat tat tat	768
Leu Leu Lys Tyr Val Ile Ile Gly Tyr Met Ile Asp Lys Tyr Tyr Tyr	
245 250 255	
aat aaa tta gta tta atc aat ata tta tcc gat aaa tta tta tct tta	816
Asn Lys Leu Val Leu Ile Asn Ile Leu Ser Asp Lys Leu Leu Ser Leu	
260 265 270	
act ata tat ttt tta aca agt gaa tat atg tat aaa tca tta aat tat	864
Thr Ile Tyr Phe Leu Thr Ser Glu Tyr Met Tyr Lys Ser Leu Asn Tyr	
275 280 285	
ttt gaa act ata gat tat tct aaa ata aaa aaa tta gaa ttt gat gat	912
Phe Glu Thr Ile Asp Tyr Ser Lys Ile Lys Lys Leu Glu Phe Asp Asp	
290 295 300	
tat gta ata tta aat gaa tat ttt gat att ata aat att tat aat aat	960
Tyr Val Ile Leu Asn Glu Tyr Phe Asp Ile Ile Asn Ile Tyr Asn Asn	
305 310 315 320	
ata aaa agt aat aat ata aat aaa tat tat tct tat tat aat aaa tat	1008
Ile Lys Ser Asn Asn Ile Asn Lys Tyr Tyr Ser Tyr Tyr Asn Lys Tyr	
325 330 335	
att gat tat att ata aat tca tct aca gat ata aat aaa ttt ttt tta	1056
Ile Asp Tyr Ile Ile Asn Ser Ser Thr Asp Ile Asn Lys Phe Phe Leu	
340 345 350	
caa ata cct aat caa cta tat tta aat aat gaa ttt gat att aat aat	1104
Gln Ile Pro Asn Gln Leu Tyr Leu Asn Asn Glu Phe Asp Ile Asn Asn	
355 360 365	
att cct gtt ttt aaa gca gaa aca tta ttt aat agt aaa ata aac aca	1152

Ile	Pro	Val	Phe	Lys	Ala	Glu	Thr	Leu	Phe	Asn	Ser	Lys	Ile	Asn	Thr		
	370					375					380						
aat	aat	aaa	aat	aaa	ata	aca	aat	att	aat	aat	ata	gaa	ata	tta	aat	1200	
Asn	Asn	Lys	Asn	Lys	Ile	Thr	Asn	Ile	Asn	Asn	Ile	Glu	Ile	Leu	Asn		
385					390				395					400			
ttt	aat	ggt	aat	aat	atg	ata	ttt	ttt	atg	aat	ggt	att	gaa	gat	aaa	1248	
Phe	Asn	Val	Asn	Asn	Met	Ile	Phe	Phe	Met	Asn	Val	Ile	Glu	Asp	Lys		
			405					410					415				
ttt	gaa	ata	aaa	aat	aat	gaa	ata	att	ata	aaa	aat	aca	aaa	aat	ata	1296	
Phe	Glu	Ile	Lys	Asn	Asn	Glu	Ile	Ile	Ile	Lys	Asn	Thr	Lys	Asn	Ile		
		420					425						430				
tat	aaa	tca	gat	aat	aat	ata	tgt	gtg	ctt	aat	aat	aat	tat	aat	tat	1344	
Tyr	Lys	Ser	Asp	Asn	Asn	Ile	Cys	Val	Leu	Asn	Asn	Asn	Tyr	Asn	Tyr		
	435						440					445					
cct	aaa	ata	tat	ttt	tat	tat	aaa	tat	ttt	ata	att	tac	ttt	ttt	tct	1392	
Pro	Lys	Ile	Tyr	Phe	Tyr	Tyr	Lys	Tyr	Phe	Ile	Ile	Tyr	Phe	Phe	Ser		
	450					455					460						
aat	ata	ttt	tta	aat	att	gac	gat	gct	ata	gaa	tat	gta	aaa	tat	aaa	1440	
Asn	Ile	Phe	Leu	Asn	Ile	Asp	Asp	Ala	Ile	Glu	Tyr	Val	Lys	Tyr	Lys		
465					470				475						480		
cct	tat	ttt	aat	tta	tta	aat	aat	att	aat	gta	gaa	aat	aat	ttt	aac	1488	
Pro	Tyr	Phe	Asn	Leu	Leu	Asn	Asn	Ile	Asn	Val	Glu	Asn	Asn	Phe	Asn		
			485					490						495			
aca	aat	ata	tta	ata	aat	aat	aaa	aaa	ata	aac	ata	aat	aca	aat	cat	1536	
Thr	Asn	Ile	Leu	Ile	Asn	Asn	Lys	Lys	Ile	Asn	Ile	Asn	Thr	Asn	His		
		500						505					510				
gat	ttc	ata	aca	gca	tta	tac	ata	tat	aat	tgt	aat	aat	aaa	aat	tgt	1584	
Asp	Phe	Ile	Thr	Ala	Leu	Tyr	Ile	Tyr	Asn	Cys	Asn	Asn	Lys	Asn	Cys		
	515					520						525					
tat	ata	cat	atg	gct	act	att	tca	gat	ata	tta	aga	gat	ctc	gga	tta	1632	
Tyr	Ile	His	Met	Ala	Thr	Ile	Ser	Asp	Ile	Leu	Arg	Asp	Leu	Gly	Leu		
	530				535					540							
ata	tac	acc	cct	att	att	aat	ttt	gaa	aat	aat	cta	ggt	tat	tta	ttt	1680	
Ile	Tyr	Thr	Pro	Ile	Ile	Asn	Phe	Glu	Asn	Asn	Leu	Val	Tyr	Leu	Phe		
545					550					555					560		
ata	ata	aca	aat	aaa	cca	cat	gaa	act	gaa	ata	cat	tta	aga	aaa	ata	1728	
Ile	Ile	Thr	Asn	Lys	Pro	His	Glu	Thr	Glu	Ile	His	Leu	Arg	Lys	Ile		
			565					570						575			
tta	aat	gat	aaa	ttt	aat	gta	aat	aat	ggt	att	aca	ata	ata	tca	aca	1776	
Leu	Asn	Asp	Lys	Phe	Asn	Val	Asn	Asn	Val	Ile	Thr	Ile	Ile	Ser	Thr		
			580					585					590				
aaa	gga	aac	tat	aac	act	aaa	gaa	tta	tta	aat	aaa	tac	ata	acc	ttc	1824	
Lys	Gly	Asn	Tyr	Asn	Thr	Lys	Glu	Leu	Leu	Asn	Lys	Tyr	Ile	Thr	Phe		

595	600	605	
aat taa			1830
Asn			
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<213>	Amsacta moorei entomopoxvirus		
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<400>	68		
atg gga gcg tcc gca agt att aat act att gtg tct gat ata act aat			48
Met Gly Ala Ser Ala Ser Ile Asn Thr Ile Val Ser Asp Ile Thr Asn			
1 5 10 15			
aga gtt gaa aat tca tta att caa aca gca aat gcc tct gca caa gca			96
Arg Val Glu Asn Ser Leu Ile Gln Thr Ala Asn Ala Ser Ala Gln Ala			
20 25 30			
ata tgt cga gta aca att gga agt att agt ttt aga tcc aca cag gga			144
Ile Cys Arg Val Thr Ile Gly Ser Ile Ser Phe Arg Ser Thr Gln Gly			
35 40 45			
tgt act ata gag gta aga aat tta tgt agt gcg caa gct gta gca caa			192
Cys Thr Ile Glu Val Arg Asn Leu Cys Ser Ala Gln Ala Val Ala Gln			
50 55 60			
gtt gac gct gta gta aat gca act att gat ttt tat aat aat tta act			240
Val Asp Ala Val Val Asn Ala Thr Ile Asp Phe Tyr Asn Asn Leu Thr			
65 70 75 80			
ttt gaa caa aaa caa gaa gca cct acg tgg ttt aca gta gct tat gga			288
Phe Glu Gln Lys Gln Glu Ala Pro Thr Trp Phe Thr Val Ala Tyr Gly			
85 90 95			
ata aat act act gta act act atc gaa aat gat ttt aga aat tta gtt			336
Ile Asn Thr Thr Val Thr Thr Ile Glu Asn Asp Phe Arg Asn Leu Val			
100 105 110			
gaa caa aga tgt aaa tct caa gct gtt tta gat agt agc ata aca gtt			384

Glu	Gln	Arg	Cys	Lys	Ser	Gln	Ala	Val	Leu	Asp	Ser	Ser	Ile	Thr	Val		
		115					120					125					
gat	aat	att	tta	gtt	aat	gat	tgt	aga	gca	cca	gga	aat	gaa	ata	gtt	432	
Asp	Asn	Ile	Leu	Val	Asn	Asp	Cys	Arg	Ala	Pro	Gly	Asn	Glu	Ile	Val		
	130					135					140						
aga	ttt	aca	ttt	gtt	aat	tct	gga	acg	gct	gct	gga	caa	tgt	gca	ata	480	
Arg	Phe	Thr	Phe	Val	Asn	Ser	Gly	Thr	Ala	Ala	Gly	Gln	Cys	Ala	Ile		
	145				150				155					160			
tct	gct	cta	tta	gat	tta	caa	gta	gcg	ggg	tct	aat	caa	gta	agt	gct	528	
Ser	Ala	Leu	Leu	Asp	Leu	Gln	Val	Ala	Gly	Ser	Asn	Gln	Val	Ser	Ala		
				165				170						175			
agt	caa	agt	caa	ggg	tta	aat	ata	gga	aat	ata	ata	tta	tat	gta	gca	576	
Ser	Gln	Ser	Gln	Gly	Leu	Asn	Ile	Gly	Asn	Ile	Ile	Leu	Tyr	Val	Ala		
			180					185					190				
ata	gca	att	att	gtt	att	gca	ata	tca	tat	gtt	tta	ata	aaa	ttt	ttt	624	
Ile	Ala	Ile	Ile	Val	Ile	Ala	Ile	Ser	Tyr	Val	Leu	Ile	Lys	Phe	Phe		
		195				200						205					
ggg	aat	aaa	cca	aca	ata	aaa	caa	caa	att	agt	tta	gaa	tta	gct	aaa	672	
Gly	Asn	Lys	Pro	Thr	Ile	Lys	Gln	Gln	Ile	Ser	Leu	Glu	Leu	Ala	Lys		
	210					215				220							
aat	gga	gca	gtg	tct	agt	caa	tta	ata	caa	tta	tcg	aga	tat	gta	tct	720	
Asn	Gly	Ala	Val	Ser	Ser	Gln	Leu	Ile	Gln	Leu	Ser	Arg	Tyr	Val	Ser		
	225				230				235					240			
aaa	ata	gat	gat	aga	gat	tga										741	
Lys	Ile	Asp	Asp	Arg	Asp												
				245													

&lt;210&gt; 69

&lt;211&gt; 831

&lt;212&gt; DNA

&lt;213&gt; Amsacta moorei entomopoxvirus

&lt;220&gt;

&lt;221&gt; exon

&lt;222&gt; (1) .. (831)

&lt;223&gt;

&lt;400&gt; 69

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Met Thr Leu Val Lys His Asn Thr Met His Asn Phe Leu His Ser Lys	
1 5 10 15	
tca aat ata tct gaa tta gat tat agt att gaa tct tcg tca gaa aga	96
Ser Asn Ile Ser Glu Leu Asp Tyr Ser Ile Glu Ser Ser Ser Glu Arg	
20 25 30	
aga gat ata att ata aaa aaa tac gat aca tta aat ata aaa aat tat	144
Arg Asp Ile Ile Ile Lys Lys Tyr Asp Thr Leu Asn Ile Lys Asn Tyr	
35 40 45	
aat aga aaa aca agt ttt aat gct ata tta ata aca agc gat aat aaa	192
Asn Arg Lys Thr Ser Phe Asn Ala Ile Leu Ile Thr Ser Asp Asn Lys	
50 55 60	
att att att gca gaa aga aaa ttt agc tat tat atg gac aca ata tat	240
Ile Ile Ile Ala Glu Arg Lys Phe Ser Tyr Tyr Met Asp Thr Ile Tyr	
65 70 75 80	
ata ata tct aca tat aaa aat ata tct gat gat ata tta gaa aca ttt	288
Ile Ile Ser Thr Tyr Lys Asn Ile Ser Asp Asp Ile Leu Glu Thr Phe	
85 90 95	
att aaa tta ttt gat aaa tta act aat aaa gaa aaa tat aat ata tat	336
Ile Lys Leu Phe Asp Lys Leu Thr Asn Lys Glu Lys Tyr Asn Ile Tyr	
100 105 110	
aat aaa aaa aga ata aat aaa aaa tat att tca att ata aat ttt att	384
Asn Lys Lys Arg Ile Asn Lys Lys Tyr Ile Ser Ile Ile Asn Phe Ile	
115 120 125	
gaa gta tat ttc gat ggt aat ata aat cat aaa tat tta caa tat tta	432
Glu Val Tyr Phe Asp Gly Asn Ile Asn His Lys Tyr Leu Gln Tyr Leu	
130 135 140	
tat aat gta aaa tct aga att ata tta aat aat aat ttt aga tac aga	480
Tyr Asn Val Lys Ser Arg Ile Ile Leu Asn Asn Asn Phe Arg Tyr Arg	
145 150 155 160	
gat aaa ttt tta att tta cct ggt ggt aaa aaa aat aat aat gaa aat	528
Asp Lys Phe Leu Ile Leu Pro Gly Gly Lys Lys Asn Asn Asn Glu Asn	
165 170 175	
att aat gaa gtt ata agt cga gaa tca cac gaa gaa ata aat att cct	576
Ile Asn Glu Val Ile Ser Arg Glu Ser His Glu Glu Ile Asn Ile Pro	
180 185 190	
ata aat aat caa gat aat aat aat att gat ata atg caa gac tat tat	624
Ile Asn Asn Gln Asp Asn Asn Asn Ile Asp Ile Met Gln Asp Tyr Tyr	
195 200 205	
tca gaa act ata ata ttt gat aaa ata ctt tca aaa aaa ttt att gat	672
Ser Glu Thr Ile Ile Phe Asp Lys Ile Leu Ser Lys Lys Phe Ile Asp	
210 215 220	
gtt act att ata gca aaa atc aaa tat agt tct att caa ata tta aat	720

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<210> 70
<211> 1002
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<213> Amsacta moorei entomopoxvirus
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<222> (1)..(1002)
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aaa aga aga aat gac aga ata aaa ata ttt tta aaa gta gaa aat aaa	288
Lys Arg Arg Asn Asp Arg Ile Lys Ile Phe Leu Lys Val Glu Asn Lys	
85 90 95	
ata cct aaa ata gaa aaa tat att aat aaa gaa ttg aat ata ttc aaa	336
Ile Pro Lys Ile Glu Lys Tyr Ile Asn Lys Glu Leu Asn Ile Phe Lys	
100 105 110	
aaa aat ggt agt aat tca tca cac ata tac ata act gat aaa atg att	384
Lys Asn Gly Ser Asn Ser Ser His Ile Tyr Ile Thr Asp Lys Met Ile	
115 120 125	
ttt gct att ata tta tta gta gaa atg tgt ttt ttt ata aga act gga	432
Phe Ala Ile Ile Leu Leu Val Glu Met Cys Phe Phe Ile Arg Thr Gly	
130 135 140	
aaa aaa aaa tat tta gaa gat aat gaa act atc gga tta ttg aca tta	480
Lys Lys Lys Tyr Leu Glu Asp Asn Glu Thr Ile Gly Leu Leu Thr Leu	
145 150 155 160	
caa aaa aat aat ttt aca ata gaa aat gat gtt ata tat ata aat ttt	528
Gln Lys Asn Asn Phe Thr Ile Glu Asn Asp Val Ile Tyr Ile Asn Phe	
165 170 175	
aaa gga aaa tta tct caa aat caa aat ttt agc ata tta aaa gat gag	576
Lys Gly Lys Leu Ser Gln Asn Gln Asn Phe Ser Ile Leu Lys Asp Glu	
180 185 190	
cat tta tta ata tac aat atg att aaa ata tta tat aat aag act aat	624
His Leu Leu Ile Tyr Asn Met Ile Lys Ile Leu Tyr Asn Lys Thr Asn	
195 200 205	
gat ttt ata ttt aaa aat agt gat gat ata ata ttt aat gaa tct aaa	672
Asp Phe Ile Phe Lys Asn Ser Asp Asp Ile Ile Phe Asn Glu Ser Lys	
210 215 220	
tta tat tct atg att aaa caa ttt aat ata aag tta aaa gat ata aga	720
Leu Tyr Ser Met Ile Lys Gln Phe Asn Ile Lys Leu Lys Asp Ile Arg	
225 230 235 240	
aca ttt gga gtt aat aga gtt tta ata caa gaa ttg tgg aaa aat gtt	768
Thr Phe Gly Val Asn Arg Val Leu Ile Gln Glu Leu Trp Lys Asn Val	
245 250 255	
aga gat tta gat att atg gat att agg cat aaa gat ata aaa aaa ata	816
Arg Asp Leu Asp Ile Met Asp Ile Arg His Lys Asp Ile Lys Lys Ile	
260 265 270	
ata tca gaa gta gtt aaa aga aca gct aat ata att ggt cat aca cca	864
Ile Ser Glu Val Val Lys Arg Thr Ala Asn Ile Ile Gly His Thr Pro	
275 280 285	
act ata tcc aaa aat agt tat ata gta gat gaa ata aga tct ata ata	912
Thr Ile Ser Lys Asn Ser Tyr Ile Val Asp Glu Ile Arg Ser Ile Ile	
290 295 300	
gat aaa gat act ata aac aaa gct aaa gaa atg aca ttt gat gaa tat	960

Asp Lys Asp Thr Ile Asn Lys Ala Lys Glu Met Thr Phe Asp Glu Tyr  
 305 310 315 320

tat aaa tat att gta gat aaa tta aaa gaa tta acc aat taa 1002  
 Tyr Lys Tyr Ile Val Asp Lys Leu Lys Glu Leu Thr Asn  
 325 330

<210> 71

<211> 1161

<212> DNA

<213> Amsacta moorei entomopoxvirus

<220>

<221> exon

<222> (1)..(1161)

<223>

<400> 71

atg ggt ggt aga gta agt ata tcg ttt ata aga cca gag aat aat aat 48  
 Met Gly Gly Arg Val Ser Ile Ser Phe Ile Arg Pro Glu Asn Asn Asn  
 1 5 10 15

aat gga aat aaa aat tta tta ata ggt tta agt gat aat aac ata gtt 96  
 Asn Gly Asn Lys Asn Leu Leu Ile Gly Leu Ser Asp Asn Asn Ile Val  
 20 25 30

aga gtt ccg atg ttt gaa caa att aat aga ata cca aga tcg gct tat 144  
 Arg Val Pro Met Phe Glu Gln Ile Asn Arg Ile Pro Arg Ser Ala Tyr  
 35 40 45

gaa aat ctc gac gaa tat gaa ata aat tat tgt att gga act cca ttt 192  
 Glu Asn Leu Asp Glu Tyr Glu Ile Asn Tyr Cys Ile Gly Thr Pro Phe  
 50 55 60

aat tct ttg gca gaa tgt gca tta tta ttt aat aat aat att ttg tct 240  
 Asn Ser Leu Ala Glu Cys Ala Leu Leu Phe Asn Asn Asn Ile Leu Ser  
 65 70 75 80

aat tat aca agc gaa tta gat aat tat gta ata act aac gaa gga tcg 288  
 Asn Tyr Thr Ser Glu Leu Asp Asn Tyr Val Ile Thr Asn Glu Gly Ser  
 85 90 95

ccg tgt act agt tta aca ttt agg ccg gga agt ata tta tat ggt aat 336  
 Pro Cys Thr Ser Leu Thr Phe Arg Pro Gly Ser Ile Leu Tyr Gly Asn  
 100 105 110

tca gaa tgg tta gaa ggt aga aca ttt gtt gga aat aaa tgt aaa ata	384
Ser Glu Trp Leu Glu Gly Arg Thr Phe Val Gly Asn Lys Cys Lys Ile	
115 120 125	
aga tat aga gga tat cca ata tat gaa aat gat ttg cgg gaa tgt tgt	432
Arg Tyr Arg Gly Tyr Pro Ile Tyr Glu Asn Asp Leu Arg Glu Cys Cys	
130 135 140	
act ggt aaa aga aca tct ggt tgt cac gaa aca tta ata aat aac ttt	480
Thr Gly Lys Arg Thr Ser Gly Cys His Glu Thr Leu Ile Asn Asn Phe	
145 150 155 160	
aca aca cca cat tgt aat gta aca atg caa aat ttt tgc aga caa aat	528
Thr Thr Pro His Cys Asn Val Thr Met Gln Asn Phe Cys Arg Gln Asn	
165 170 175	
ccg gaa gat tta tat tgc tat aga tgg atg tat agc caa tct aaa aca	576
Pro Glu Asp Leu Tyr Cys Tyr Arg Trp Met Tyr Ser Gln Ser Lys Thr	
180 185 190	
ttt gat att gct tta aaa tta tat tca gaa tta tgt agt ata gat cat	624
Phe Asp Ile Ala Leu Lys Leu Tyr Ser Glu Leu Cys Ser Ile Asp His	
195 200 205	
act aaa tta tat tgt gat tat atg tgt gtg tat gcg aga gaa aat gga	672
Thr Lys Leu Tyr Cys Asp Tyr Met Cys Val Tyr Ala Arg Glu Asn Gly	
210 215 220	
tat cca gga tat tgt gat gat tcg ttg tca aac tgg tgt aaa aat aat	720
Tyr Pro Gly Tyr Cys Asp Asp Ser Leu Ser Asn Trp Cys Lys Asn Asn	
225 230 235 240	
agt aat aat tcg tta tgt ttt tgt tat aat cct cct act gaa ttt ata	768
Ser Asn Asn Ser Leu Cys Phe Cys Tyr Asn Pro Pro Thr Glu Phe Ile	
245 250 255	
cca gat gtt gaa gaa gtt ttg ggt cca aaa gaa tgt tgg tta gcg cca	816
Pro Asp Val Glu Glu Val Leu Gly Pro Lys Glu Cys Trp Leu Ala Pro	
260 265 270	
tgt act gtc tct tat agt ggt caa aaa tgg tta aca acc aat cag atg	864
Cys Thr Val Ser Tyr Ser Gly Gln Lys Trp Leu Thr Thr Asn Gln Met	
275 280 285	
aat ata aaa aaa aat tgt aat ata caa tct tgt att ata acc ata gga	912
Asn Ile Lys Lys Asn Cys Asn Ile Gln Ser Cys Ile Ile Thr Ile Gly	
290 295 300	
tca ttg tta act aga ggt aat aat aaa att gat tta ata aat aat tgt	960
Ser Leu Leu Thr Arg Gly Asn Asn Lys Ile Asp Leu Ile Asn Asn Cys	
305 310 315 320	
ata aac aat tta aac gca agc aca gta ata aat tca gaa aat tta tca	1008
Ile Asn Asn Leu Asn Ala Ser Thr Val Ile Asn Ser Glu Asn Leu Ser	
325 330 335	
aat gtc act gat ata aaa ata aat caa aca tgg gga gta ttt ttc gat	1056

Asn Val Thr Asp Ile Lys Ile Asn Gln Thr Trp Gly Val Phe Phe Asp	
340 345 350	
cct gtt ata ttt att tta ata ata ttt ata ttt ata ttg ata ata tta	1104
Pro Val Ile Phe Ile Leu Ile Ile Phe Ile Phe Ile Leu Ile Ile Leu	
355 360 365	
tat ttt tat aat aaa aaa cca ata tat act att aat ata agt gaa act	1152
Tyr Phe Tyr Asn Lys Lys Pro Ile Tyr Thr Ile Asn Ile Ser Glu Thr	
370 375 380	
aat tta taa	1161
Asn Leu	
385	
<210> 72	
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<213> Amsacta moorei entomopoxvirus	
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<221> exon	
<222> (1) .. (423)	
<223>	
<400> 72	
atg tta agt aat tat gaa aat gat aat aaa atg ata gaa tat tgt aat	48
Met Leu Ser Asn Tyr Glu Asn Asp Asn Lys Met Ile Glu Tyr Cys Asn	
1 5 10 15	
aat aat aaa gat gat ata aaa tgt caa tgt tta ata gtg aat gat aat	96
Asn Asn Lys Asp Asp Ile Lys Cys Gln Cys Leu Ile Val Asn Asp Asn	
20 25 30	
atc gat gta ttt tca aaa tca tca tat gcg cca tat ttt tgt tgg tat	144
Ile Asp Val Phe Ser Lys Ser Ser Tyr Ala Pro Tyr Phe Cys Trp Tyr	
35 40 45	
tct gcg tgt aga aat aat gaa aac tat att act agt tta ata aaa agt	192
Ser Ala Cys Arg Asn Asn Glu Asn Tyr Ile Thr Ser Leu Ile Lys Ser	
50 55 60	
gaa caa caa tat tgt aat att aca gtg tgt gaa att agt gtt aca gat	240
Glu Gln Gln Tyr Cys Asn Ile Thr Val Cys Glu Ile Ser Val Thr Asp	
65 70 75 80	

ata gta tta aat gac aat gga aat tta act gta aca aac gaa tgt gct	288
Ile Val Leu Asn Asp Asn Gly Asn Leu Thr Val Thr Asn Glu Cys Ala	
85 90 95	
agt aac ata aat cct ata tat tca tta tct caa att ata gtt aat tta	336
Ser Asn Ile Asn Pro Ile Tyr Ser Leu Ser Gln Ile Ile Val Asn Leu	
100 105 110	
acg tca ttt gac ata cca aat tta ttt gta agt ttt ttt tat ccg ata	384
Thr Ser Phe Asp Ile Pro Asn Leu Phe Val Ser Phe Phe Tyr Pro Ile	
115 120 125	
gtt att att ata tca att tta ata ttt ttt aaa aaa taa	423
Val Ile Ile Ile Ser Ile Leu Ile Phe Phe Lys Lys	
130 135 140	

&lt;210&gt; 73

&lt;211&gt; 747

&lt;212&gt; DNA

&lt;213&gt; Amsacta moorei entomopoxvirus

&lt;220&gt;

&lt;221&gt; exon

&lt;222&gt; (1) .. (747)

&lt;223&gt;

<400> 73	
atg aat gaa tcg caa tta caa acc aga aat agt agt att aat ata ggt	48
Met Asn Glu Ser Gln Leu Gln Thr Arg Asn Ser Ser Ile Asn Ile Gly	
1 5 10 15	
aga act ata ttt aat gac gta tat act aga ttt atc gat aaa tta aat	96
Arg Thr Ile Phe Asn Asp Val Tyr Thr Arg Phe Ile Asp Lys Leu Asn	
20 25 30	
aga ata tct agt aca aca aat att aat tgt aat ata aat ata aat gaa	144
Arg Ile Ser Ser Thr Thr Asn Ile Asn Cys Asn Ile Asn Ile Asn Glu	
35 40 45	
ata aga aca agt aat att aat aat tgt aat ata gtt tta agt aat aaa	192
Ile Arg Thr Ser Asn Ile Asn Asn Cys Asn Ile Val Leu Ser Asn Lys	
50 55 60	
tgt gtt agt aat gaa ata act agt ttt aca tta tta tta caa agt tta	240
Cys Val Ser Asn Glu Ile Thr Ser Phe Thr Leu Leu Leu Gln Ser Leu	
65 70 75 80	

gga gaa act atg tta cta tta cca gaa gac aga cgc aca caa ata gaa 288  
 Gly Glu Thr Met Leu Leu Leu Pro Glu Asp Arg Arg Thr Gln Ile Glu  
 85 90 95

aat ata tta gga ata tcc aca gat gat ata ata aat gaa aat gat act 336  
 Asn Ile Leu Gly Ile Ser Thr Asp Asp Ile Ile Asn Glu Asn Asp Thr  
 100 105 110

gga ttc ata aat aat tgt aga gca agt gca gta gtg gac aat agt ata 384  
 Gly Phe Ile Asn Asn Cys Arg Ala Ser Ala Val Val Asp Asn Ser Ile  
 115 120 125

aat atc ggt act ata gaa ata aat gat tgt tat tct aat ttt cct act 432  
 Asn Ile Gly Thr Ile Glu Ile Asn Asp Cys Tyr Ser Asn Phe Pro Thr  
 130 135 140

gat ttc tta ttt tta aat gcg ggt tct gcg gat gct aat tgt gga ata 480  
 Asp Phe Leu Phe Leu Asn Ala Gly Ser Ala Asp Ala Asn Cys Gly Ile  
 145 150 155 160

aaa tat ata tca gat gca tta cta aaa tta gat aat aga aaa cca gaa 528  
 Lys Tyr Ile Ser Asp Ala Leu Leu Lys Leu Asp Asn Arg Lys Pro Glu  
 165 170 175

tta tca ttg caa tta ttg ttt aat ata aaa atg ata gat tat ata ata 576  
 Leu Ser Leu Gln Leu Leu Phe Asn Ile Lys Met Ile Asp Tyr Ile Ile  
 180 185 190

ata tta ata act att tta tct ata tat ata tta ttt att ttt atg tca 624  
 Ile Leu Ile Thr Ile Leu Ser Ile Tyr Ile Leu Phe Ile Phe Met Ser  
 195 200 205

ttt tta ata cca aga aat aaa aaa tct atc tat tat tct aga aat act 672  
 Phe Leu Ile Pro Arg Asn Lys Lys Ser Ile Tyr Tyr Ser Arg Asn Thr  
 210 215 220

att ctt aat aaa aat gat aaa atc tta gaa aat att tat ttg aga cat 720  
 Ile Leu Asn Lys Asn Asp Lys Ile Leu Glu Asn Ile Tyr Leu Arg His  
 225 230 235 240

tac gat ggg atc aat aat ttt ata tga 747  
 Tyr Asp Gly Ile Asn Asn Phe Ile  
 245

<210> 74

<211> 1011

<212> DNA

<213> Amsacta moorei entomopoxvirus

&lt;220&gt;

&lt;221&gt; exon

&lt;222&gt; (1)..(1011)

&lt;223&gt;

&lt;400&gt; 74

atg gga ggc agt gtt gac atc gaa gct aga tat act ggt tcc tct aat	48
Met Gly Gly Ser Val Asp Ile Glu Ala Arg Tyr Thr Gly Ser Ser Asn	
1 5 10 15	
ttt caa gaa aca tat ttg tca ttt tca aat tta att aat act ata tat	96
Phe Gln Glu Thr Tyr Leu Ser Phe Ser Asn Leu Ile Asn Thr Ile Tyr	
20 25 30	
ata tta aca aga gat gaa aga ata cca ata ggt ata ttt tca aac aat	144
Ile Leu Thr Arg Asp Glu Arg Ile Pro Ile Gly Ile Phe Ser Asn Asn	
35 40 45	
cct gat gat tac aga aat tat cga gga tat act gct ata ttt aaa cca	192
Pro Asp Asp Tyr Arg Asn Tyr Arg Gly Tyr Thr Ala Ile Phe Lys Pro	
50 55 60	
ggc gga tat aaa gaa tta ttg aaa gta aat gac tta gga ccc gat gac	240
Gly Gly Tyr Lys Glu Leu Lys Val Asn Asp Leu Gly Pro Asp Asp	
65 70 75 80	
ttg tgt tgt att tat gat tgg aga tat gct tgg gtt gat gaa aat aat	288
Leu Cys Cys Ile Tyr Asp Trp Arg Tyr Ala Trp Val Asp Glu Asn Asn	
85 90 95	
ata tta tca caa aac gca agt gta aat aaa aat tta ttt acg tgc gat	336
Ile Leu Ser Gln Asn Ala Ser Val Asn Lys Asn Leu Phe Thr Cys Asp	
100 105 110	
cct aga act ata caa gta gga act aat aat att tgt gat aat tcg atg	384
Pro Arg Thr Ile Gln Val Gly Thr Asn Asn Ile Cys Asp Asn Ser Met	
115 120 125	
tat aga gct tgt ata tta gat ttt aat aat cat aga tat tta gaa gcg	432
Tyr Arg Ala Cys Ile Leu Asp Phe Asn Asn His Arg Tyr Leu Glu Ala	
130 135 140	
aaa tgt ggt gtt tgg tta gat ggt tta ttt aaa aga ttt gca aca gct	480
Lys Cys Gly Val Trp Leu Asp Gly Leu Phe Lys Arg Phe Ala Thr Ala	
145 150 155 160	
tca aat att ata aat aat aca aat aat ata cta tta caa tcg tgt tct	528
Ser Asn Ile Ile Asn Asn Thr Asn Asn Ile Leu Leu Gln Ser Cys Ser	
165 170 175	
aat aat att aat aat gat ttg tgt ata aaa tgg tta ata gca ata aga	576
Asn Asn Ile Asn Asn Asp Leu Cys Ile Lys Trp Leu Ile Ala Ile Arg	

180	185	190	
aat agc gga aat cct aca ttt ttt tca tta gca gat aat gtt tta aac			624
Asn Ser Gly Asn Pro Thr Phe Phe Ser Leu Ala Asp Asn Val Leu Asn			
195	200	205	
gca caa aca gat aaa aca aat tta aaa tgt gct ttt tct cct tca tat			672
Ala Gln Thr Asp Lys Thr Asn Leu Lys Cys Ala Phe Ser Pro Ser Tyr			
210	215	220	
att aca gat aca caa aat aga tta aat gtt cca aaa gaa tgt tgg tat			720
Ile Thr Asp Thr Gln Asn Arg Leu Asn Val Pro Lys Glu Cys Trp Tyr			
225	230	235	240
aga gag tgt gct ttt tca cca aat tat cta tta tta act gac aat ata			768
Arg Glu Cys Ala Phe Ser Pro Asn Tyr Leu Leu Leu Thr Asp Asn Ile			
245	250	255	
aca tta aaa aat aat tgt tca ttg tct gaa tgt aat ata aat atc gga			816
Thr Leu Lys Asn Asn Cys Ser Leu Ser Glu Cys Asn Ile Asn Ile Gly			
260	265	270	
aat tta gat ata gta tct gcg tca gaa gta aca ata act tgc aat aat			864
Asn Leu Asp Ile Val Ser Ala Ser Glu Val Thr Ile Thr Cys Asn Asn			
275	280	285	
aat aaa tca aat act gta tca tca aga caa aaa tta gat ata tta ttg			912
Asn Lys Ser Asn Thr Val Ser Ser Arg Gln Lys Leu Asp Ile Leu Leu			
290	295	300	
aga gaa tca gaa gat tat aga ttt ttg tta act aac aac att tta ata			960
Arg Glu Ser Glu Asp Tyr Arg Phe Leu Leu Thr Asn Asn Ile Leu Ile			
305	310	315	320
tta att tta tta ttt ata ttt tta ata ttt tta ata att aga cat aat			1008
Leu Ile Leu Leu Phe Ile Phe Leu Ile Phe Leu Ile Ile Arg His Asn			
325	330	335	
taa			1011

&lt;210&gt; 75

&lt;211&gt; 293

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; HaEPV from Figure 10

&lt;400&gt; 75



Met Ser Phe Asn Pro Ile Ile Tyr Tyr Ile Ser Asp Ile Lys Asn Glu  
1 5 10 15

Arg Pro Tyr Lys Lys Asn Thr Lys Pro Tyr Ile Phe Asn Phe Arg Lys  
20 25 30

Pro Gly Gln Ile Lys Leu Leu Ile Asn Glu Ile Arg Phe Leu Thr Glu  
35 40 45

Asp Val Glu Ile Tyr Lys Asn Tyr Asn Asn Lys Ile Ile Asn Ile Leu  
50 55 60

Tyr Ile Gly Ser Gly Lys Gly Tyr His Ile Pro Leu Leu Met Glu Ile  
65 70 75 80

Tyr Ser Lys Tyr Asn Ile Ile Trp His Leu Tyr Asp Pro Asn Gly His  
85 90 95

Cys Asp Lys Leu Asn Glu Ile Ser Asn Lys Asn Asn Asn Val Asn Ile  
100 105 110

Tyr Asn Gln Ile Phe Asp Lys Lys Asp Val Glu Leu Tyr Glu Asp Val  
115 120 125

Gln Asn Leu Leu Phe Ile Ser Asp Ile Arg Thr Ile Asp Asp Asp Lys  
130 135 140

Ile Glu Pro Asn Thr Lys Asn Leu Ile His Asp Tyr Asp Ile Gln Asn  
145 150 155 160

Tyr Val Leu Lys Gln Leu Lys Pro Ile Ala Leu Ile Lys Gln Arg Asp  
165 170 175

Pro Phe Pro Asn Asp Trp Asp Glu Ser Tyr Glu Met Tyr Ile Pro Asp  
180 185 190

Gly Lys Glu Tyr Val Gln Cys Phe Gln Lys His Asp Ser Ala Glu Tyr  
195 200 205

Arg Ile Phe Val Cys Gly Ala Thr Thr Phe Thr Lys Val Asn Leu Asp  
210 215 220

Val Leu Lys Thr Arg Asn Ile Asp Lys Lys Leu Ala Trp Tyr Asn Thr

Met	Ser	Ile	Tyr	Met	Lys	Ile	Asn	Asp	Phe	Lys	Lys	Pro	Asn	Val	Leu
1				5					10					15	
Ile	Phe	Asp	Asn	Ile	Asn	Asn	Gln	Leu	Lys	Tyr	Lys	Pro	Asn	Asn	Val
			20					25					30		
Ser	Asn	Lys	His	Pro	Gly	Gln	Leu	Lys	Leu	Leu	Met	Thr	Glu	Leu	Gln
		35					40					45			
Phe	Phe	Asn	Asn	Cys	Asn	Ile	Asp	Ala	Leu	Asn	Ser	Lys	Asp	Arg	Pro
	50					55					60				
Ile	Tyr	Val	Leu	Tyr	Ile	Gly	Ser	Gly	Arg	Gly	Tyr	His	Leu	Ile	Lys
65					70					75					80
Leu	Leu	Asp	Leu	Tyr	Lys	Asp	Tyr	Asn	Ile	Lys	Trp	Tyr	Phe	Tyr	Asp
				85					90					95	

Pro Ser Gly His Cys Ile Ser Leu Glu Arg Met Ser Gln Tyr Val Ser  
                   100                  105                  110

Ile Asn Asn Asp Tyr Phe Thr Glu Lys Asn Ile Asn Glu Phe Lys Asn  
                   115                  120                  125

Lys Lys Pro Leu Leu Phe Ile Ser Asp Ile Arg Ser Thr Asp Gly Ser  
           130                  135                  140

Glu Pro Arg Thr Lys Asn Leu Ile Asp Asp Tyr Lys Ile Gln Asn Asn  
   145                  150                  155                  160

Ile Val Leu Asn Leu Arg Pro Leu Tyr Ser Leu Leu Lys Phe Arg Tyr  
                   165                  170                  175

Pro Phe Pro Asp Asp Phe Pro Pro Glu Ile Glu Asn Glu Val Tyr Val  
                   180                  185                  190

Asp Gly Ile Lys Phe Leu Gln Pro Phe Cys Gly Pro Gln Ser Thr Glu  
           195                  200                  205

Met Arg Ile Phe Val Ser Glu Gln Asn Ile Ile Leu Lys Asn Phe Ser  
       210                  215                  220

Lys Glu Glu Ser Ile Leu Phe Glu Glu Lys Met Tyr Tyr Tyr Asn Lys  
   225                  230                  235                  240

Asn Tyr Arg Ile Ile Asn Lys Asn Asp Ile Leu Ile Ala Gly Phe Ile  
                   245                  250                  255

Leu Lys Ser Thr Asn Lys Phe Asp Asn Met Lys Tyr Ile Asp Ile Ile  
                   260                  265                  270

Lys Ser Leu Glu Asn Ser Ile Asn Asn Gln Ile Arg Glu Asp Ile Ser  
           275                  280                  285

Phe Asn Lys Leu Asp Ile Lys  
       290                  295

<210> 77

&lt;211&gt; 333

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; VVJ3R from Figure 10

&lt;400&gt; 77

Met Asp Val Val Ser Leu Asp Lys Pro Phe Met Tyr Phe Glu Glu Ile  
 1 5 10 15

Asp Asn Glu Leu Asp Tyr Glu Pro Glu Ser Ala Asn Glu Val Ala Lys  
 20 25 30

Lys Leu Pro Tyr Gln Gly Gln Leu Lys Leu Leu Leu Gly Glu Leu Phe  
 35 40 45

Phe Leu Ser Lys Leu Gln Arg His Gly Ile Leu Asp Gly Ala Thr Val  
 50 55 60

Val Tyr Ile Gly Ser Ala Pro Gly Thr His Ile Arg Tyr Leu Arg Asp  
 65 70 75 80

His Phe Tyr Asn Leu Gly Met Ile Ile Lys Trp Met Leu Ile Asp Gly  
 85 90 95

Arg His His Asp Pro Ile Leu Asn Gly Leu Arg Asp Val Thr Leu Val  
 100 105 110

Thr Arg Phe Val Asp Glu Glu Tyr Leu Arg Ser Ile Lys Lys Gln Leu  
 115 120 125

His Pro Ser Lys Ile Ile Leu Ile Ser Asp Val Arg Ser Lys Arg Gly  
 130 135 140

Gly Asn Glu Pro Ser Thr Ala Asp Leu Leu Ser Asn Tyr Ala Leu Gln  
 145 150 155 160

Asn Val Met Ile Ser Ile Leu Asn Pro Val Ala Ser Ser Leu Lys Trp  
 165 170 175

Arg Cys Pro Phe Pro Asp Gln Trp Ile Lys Asp Phe Tyr Ile Pro His  
                   180                                  185                                  190

Gly Asn Lys Met Leu Gln Pro Phe Ala Pro Ser Tyr Ser Ala Glu Met  
                   195                                  200                                  205

Arg Leu Leu Ser Ile Tyr Thr Gly Glu Asn Met Arg Leu Thr Arg Val  
                   210                                  215                                  220

Thr Lys Ser Asp Val Val Asn Tyr Glu Lys Lys Met Tyr Tyr Leu Asn  
                   225                                  230                                  235                                  240

Lys Ile Val Arg Asn Lys Val Val Val Asn Phe Asp Tyr Pro Asn Gln  
                                   245                                  250                                  255

Glu Tyr Asp Tyr Phe His Met Tyr Phe Met Leu Arg Thr Val Tyr Cys  
                                   260                                  265                                  270

Asn Lys Thr Phe Pro Thr Thr Lys Ala Lys Val Leu Phe Leu Gln Gln  
                   275                                  280                                  285

Ser Ile Phe Arg Phe Leu Asn Ile Pro Thr Thr Ser Thr Glu Lys Val  
                   290                                  295                                  300

Ser His Glu Pro Ile Gln Arg Lys Ile Ser Ser Lys Asn Ser Met Ser  
                   305                                  310                                  315                                  320

Lys Asn Arg Asn Ser Lys Arg Ser Val Arg Gly Asn Lys  
                                   325                                  330

<210> 78

<211> 30

<212> PRT

<213> Artificial Sequence

<220>

<223> Consensus from Figure 10

<400> 78

Pro Asn Tyr Leu Phe Tyr Ile Gly Ser His Leu Ile Trp Asp Ile Asp  
 1 5 10 15

Leu Tyr Gln Asn Leu Pro Lys Gly Ser Arg Lys Asn Asn Tyr  
 20 25 30

<210> 79

<211> 46

<212> PRT

<213> Artificial Sequence

<220> .

<223> Insect Cons from Figure 10

<400> 79

Pro Asn Tyr Leu Phe Asn Leu Tyr Ile Gly Ser Tyr His Leu Tyr Ile  
 1 5 10 15

Trp Tyr Asp Cys Phe Leu Ile Asp Leu Tyr Gln Asn Leu Pro Leu Lys  
 20 25 30

Gly Ser Arg Lys Tyr Asn Asn Asp Ile Leu Asn Tyr Ile Lys  
 35 40 45

<210> 80

<211> 80

<212> PRT

<213> Artificial Sequence

<220>

<223> AmEPV Cons from Figure 10

<400> 80

Pro Tyr Tyr Asp Asn Tyr Asp Asn Asn Lys Lys Leu Ile Phe Leu Asn  
 1 5 10 15

Asn Asn Ile Leu Tyr Ile Gly Ser Lys Tyr His Leu Tyr Ile Gln Trp

20

25

30

Tyr Asp Cys Asn Ile Phe Asp Leu Ile Asp Asp Asp Asn Leu Tyr Gln  
35 40 45

Asn Ile Leu Pro Ser Leu Lys Asn Trp Ser Gly Tyr Ser Arg Ile Lys  
50 55 60

Tyr Asn Asn Asp Ile Ile Leu Asn Lys Asn Tyr Asn Ile Lys Lys Ile  
65 70 75 80